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<221> misc_feature
<222> 161-163, 187-190 and 253-256
<223> N-glycosylation Sites.

<400> 10
Met Leu Phe Trp Val Leu Gly Leu Leu Ile Leu Cys Gly Phe Leu
1 5 10 15
Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys
20 25 30
Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala
35 40 45
Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys
50 55 60
Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu
65 70 75
Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val
80 85 90
Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly
95 100 105
Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala
110 115 120
Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu
125 130 135
Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro
140 145 150
Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val
155 160 165
Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr Thr Pro Ser Lys
170 175 180
Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys
185 190 195

Ala Phe Gly Val	His Val Ser Cys Ile	Glu Pro Gly Leu Phe	Lys
200		205	210
Thr Asn Leu Ala	Asp Pro Val Lys Val	Ile Glu Lys Lys.Leu	Ala
215		220	225
Ile Trp Glu Gln	Leu Ser Pro Asp Ile	Lys Gln Gln Tyr Gly	Glu
230		235	240
Gly Tyr Ile Glu	Lys Ser Leu Asp Lys	Leu Lys Gly Asn Lys	Ser
245		250	255
Tyr Val Asn Met	Asp Leu Ser Pro Val	Val Glu Cys Met Asp	His
260		265	270
Ala Leu Thr Ser	Leu Phe Pro Lys Thr	His Tyr Ala Ala Gly	Lys
275		280	285
Asp Ala Lys Ile	Phe Trp Ile Pro Leu	Ser His Met Pro Ala	Ala
290		295	300
Leu Gln Asp Phe	Leu Leu Leu Lys Gln	Lys Ala Glu Leu Ala	Asn
305		310	315
Pro Lys Ala Val			

<210> 11
 <211> 2720
 <212> DNA
 <213> Homo sapiens

<400> 11
 gcgggctggt gacggcgctg cgatggctgc ctgcgagggc aggagaagcg 50
 gagctctcgg ttcctctcag tcggacttcc tgacgccgcc agtgggagggg 100
 gcccttggg ccgtcgccac cactgtagtc atgtaccac cgccgccgcc 150
 gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200
 atgacaacag caagagtgg cggcggcgct cgtgctggag gaaatggaag 250
 caactgtcga gattgcagcg gaatatgatt ctcttctctc ttgcctttct 300
 gcttttctgt ggactcctct tctacatcaa cttgggtgac cattggaaag 350
 ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400
 gggttaaaac cagcaaattc acccgcttta ccagctctc agaaggcgga 450
 caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500
 acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550
 ctgaaggatg ggaccagga ggaggccaca aaaaggcaag aagcccctgt 600
 ggatccccgc ccggaaggag atccgcagag gacagtcac agctggaggg 650

gagcgggtgat cgagcctgag cagggcaccg agctcccttc aagaagagca 700
gaagtgccca ccaagcctcc cctgccaccg gccaggacac agggcacacc 750
agtgcattctg aactatcgcc agaagggcgt gattgacgtc ttcttgcattg 800
catggaaagg ataccgcaag ttctgcatggg gccatgacga gctgaagcct 850
gtgtccagggt ccttcagtga gtgggtttggc ctcggtctca cactgatcga 900
cgcgctggac accatgtgga tcttgggtct gaggaagaa tttgaggaag 950
ccaggaagtg ggtgtcgaag aagttacact ttgaaaagga cgtggacgtc 1000
aacctgtttg agagcacgat ccgcatcctg ggggggctcc tgagtgccta 1050
ccacctgtct ggggacagcc tcttctctgag gaaagctgag gattttggaa 1100
atcggttaat gcctgccttc agaacacat ccaagattcc ttactcggat 1150
gtgaacatcg gtactggagt tgcccacccg ccacggtgga cctccgacag 1200
cactgtggcc gaggtgacca gcattcagct ggagttcccg gagctctccc 1250
gtctcacagg ggataagaag ttctcaggagg cagtggagaa ggtgacacag 1300
cacatccacg gcctgtctgg gaagaaggat gggctggtgc ccatgttcat 1350
caatacccac agtggcctct tcacccacct gggcgtattc acgctgggag 1400
ccagggccga cagctactat gactacctgc tgaagcagtg gatccagggc 1450
gggaagcagg agacacagct gctggaagac tacgtggaag ccatcgaggg 1500
tgtcagaacg cacctgctgc ggcactccga gccagtaag ctacaccttg 1550
tggggggagct tgcccacggc cgcttcagtg ccaagatgga ccacctggtg 1600
tgcttctctg cagggacgct ggctctgggc gtctaccacg gcctgcccgc 1650
cagccacatg gagctggccc aggagctcat ggagacttgt taccagatga 1700
accggcagat ggagacgggg ctgagtcccg agatcgtgca cttcaacctt 1750
tacccccagc cgggccgctg ggacgtggag gtcaagccag cagacaggca 1800
caacctgctg cggccagaga ccgtggagag cctgttctac ctgtaccgag 1850
tcacagggga ccgcaaatac caggactggg gctgggagat tctgcagagc 1900
ttcagccgat tcacacgggt cccctcgggt ggctattctt ccatcaacaa 1950
tgtccaggat cctcagaagc ccgagcctag ggacaagatg gagagcttct 2000
tcctggggga gacgctcaag tatctgttct tgctcttctc cgatgacca 2050
aacctgctca gcctggacgc ctacgtgttc aacaccgaag cccacctct 2100

gcctatctgga acccctgcct aggggtggatg gctgctggtg tggggacttc 2150
 ggggtgggcag aggcaccttg ctgggtctgt ggcattttcc aaggggccac 2200
 gtagcaccgg caaccgcaa gtggcccagg ctctgaactg gctctgggct 2250
 cctcctcgtc tctgctttaa tcaggacacc gtgaggacaa gtgaggccgt 2300
 cagtcttggt gtgatgcggg gtgggctggg ccgctggagc ctccgcctgc 2350
 ttctccaga agacacgaat catgactcac gattgctgaa gcctgagcag 2400
 gtctctgtgg gccgaccaga ggggggcttc gaggtggtcc ctggtactgg 2450
 ggtgaccgag tggacagccc aggggtgcagc tctgcccggg ctctggaagc 2500
 ctcatatgct cccaatccaa ggggtctggag gggctgccgt gactccagag 2550
 gcctgaggct ccagggtctg ctctggtgtt tacaagctgg actcagggat 2600
 cctcctggcc gcccgcagg gggcttggag ggctggacgg caagtccgtc 2650
 tagctcacgg gccctccag tggaatgggt cttttcggtg gagataaaag 2700
 ttgatttgc ctaaccgcaa 2720

<210> 12
 <211> 699
 <212> PRT
 <213> Homo sapiens

<220>
 <221> TRANSMEM
 <222> 21-40 and 84-105
 <223> Transmembrane Domain (type II)

<400> 12
 Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser
 1 5 10 15
 Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala
 20 25 30
 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro Pro
 35 40 45
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr
 50 55 60
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp
 65 70 75
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
 80 85 90
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
 95 100 105

[illegible]

395					400					405						
Arg	Glu	Leu	Ser	410	Arg	Leu	Thr	Gly	Asp	Lys	Lys	Phe	Gln	Glu	Ala	420
Val	Glu	Lys	Val	425	Thr	Gln	His	Ile	His	Gly	Leu	Ser	Gly	Lys	Lys	435
Asp	Gly	Leu	Val	440	Pro	Met	Phe	Ile	Asn	Thr	His	Ser	Gly	Leu	Phe	450
Thr	His	Leu	Gly	455	Val	Phe	Thr	Leu	Gly	Ala	Arg	Ala	Asp	Ser	Tyr	465
Tyr	Glu	Tyr	Leu	470	Leu	Lys	Gln	Trp	Ile	Gln	Gly	Gly	Lys	Gln	Glu	480
Thr	Gln	Leu	Leu	485	Glu	Asp	Tyr	Val	Glu	Ala	Ile	Glu	Gly	Val	Arg	495
Thr	His	Leu	Leu	500	Arg	His	Ser	Glu	Pro	Ser	Lys	Leu	Thr	Phe	Val	510
Gly	Glu	Leu	Ala	515	His	Gly	Arg	Phe	Ser	Ala	Lys	Met	Asp	His	Leu	525
Val	Cys	Phe	Leu	530	Pro	Gly	Thr	Leu	Ala	Leu	Gly	Val	Tyr	His	Gly	540
Leu	Pro	Ala	Ser	545	His	Met	Glu	Leu	Ala	Gln	Glu	Leu	Met	Glu	Thr	555
Cys	Tyr	Gln	Met	560	Asn	Arg	Gln	Met	Glu	Thr	Gly	Leu	Ser	Pro	Glu	570
Ile	Val	His	Phe	575	Asn	Leu	Tyr	Pro	Gln	Pro	Gly	Arg	Arg	Asp	Val	585
Glu	Val	Lys	Pro	590	Ala	Asp	Arg	His	Asn	Leu	Leu	Arg	Pro	Glu	Thr	600
Val	Glu	Ser	Leu	605	Phe	Tyr	Leu	Tyr	Arg	Val	Thr	Gly	Asp	Arg	Lys	615
Tyr	Gln	Asp	Trp	620	Gly	Trp	Glu	Ile	Leu	Gln	Ser	Phe	Ser	Arg	Phe	630
Thr	Arg	Val	Pro	635	Ser	Gly	Gly	Tyr	Ser	Ser	Ile	Asn	Asn	Val	Gln	645
Asp	Pro	Gln	Lys	650	Pro	Glu	Pro	Arg	Asp	Lys	Met	Glu	Ser	Phe	Phe	660
Leu	Gly	Glu	Thr	665	Leu	Lys	Tyr	Leu	Phe	Leu	Leu	Phe	Ser	Asp	Asp	675
Pro	Asn	Leu	Leu	680	Ser	Leu	Asp	Ala	Tyr	Val	Phe	Asn	Thr	Glu	Ala	690

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tcccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
ggcgccgctg agggccggga ggccggggccg gccgggctgc gagcgccctgc 50
cccatgcgcc gccgcctctc cgcacgatgt tcccctcgcg gaggaagcgc 100
gcgcagctgc cctgggagga cggcaggtcc ggggttgctct ccggcggcct 150
ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgtg 200
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

```

cgggcagtca ggggacaagg gcaggagacc tcgggccctc cccgtgcctg 300
ccccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350
cccaccgcct ggcagtgctg gtgcccttcc gcgaacgctt cgaggagctc 400
ctggtcttcg tgccccacat gcgccgcttc ctgagcagga agaagatccg 450
gcaccacatc tacgtgctca accaggtgga ccacttcagg ttcaaccggg 500
cagcgctcat caacgtgggc ttccctggaga gcagcaacag cacggactac 550
attgccatgc acgacgttga cctgctccct ctcaacgagg agctggacta 600
tggttttcc cctggtgggc ccttccacgt ggcctccccg gagctccacc 650
ctctctacca ctacaagacc tatgtcggcg gcctcctgct gctctccaag 700
cagcactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggctgggg 750
ccgcgaggac gacgagttct accggcgcat taaggagct gggctccagc 800
ttttccgccc ctcggaatc acaactgggt acaagacatt tcgccacctg 850
catgaccag cctggcgga gagggaccag aagcgcatcg cagctcaaaa 900
acaggagcag ttcaaggtgg acaggaggag aggcctgaac actgtgaagt 950
accatgtggc ttcccgcact gccctgtctg tgggcggggc cccctgcact 1000
gtcctcaaca tcatgttga ctgtgacaag accgccacac cctggtgcac 1050
attcagctga gctggatgga cagtgaggaa gcctgtacct acaggccata 1100
ttgctcaggc tcaggacaag gcctcaggtc gtgggcccag ctctgacagg 1150
atgtggagtg gccaggacca agacagcaag ctacgcaatt gcagccaccc 1200
ggccgccaag gcaggcttgg gctgggccag gacacgtggg gtgcctggga 1250
cgctgcttgc catgcacagt gatcagagag aggctggggt gtgtcctgtc 1300
cgggaccccc cctgccttcc tgctcacctt actctgacct ccttcacgtg 1350
cccaggcctg tgggtagtgg ggagggtga acaggacaac ctctcatcac 1400
cctactctga cctccttcac gtgccaggc ctgtgggtag tggggagggc 1450
tgaacaggac aacctctcat ccccccaaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaaaaaaa aaaaaaaaaa aaaa 1524

```

```

<210> 17
<211> 327
<212> PRT
<213> Homo sapiens
<220>

```

[illegible]

```
<220>
<221> misc feature
<222> 19-25,65-71,247-253,285-291,303-310
<223> N-myristoylation site.
```

```
<220>
<221> misc_feature
<222> 27-31
<223> cAMP- and cGMP-dependent protein kinase phosphorylation site.
```

```
<220>
<221> TRANSMEM
<222> 29-49
<223> Transmembrane domain (type II).
```

```
<220>
<221> misc_feature
<222> 154-158
<223> N-glycosylation site.
```

```
<220>
<221> misc_feature
<222> 226-233
<223> Tyrosine kinase phosphorylation site.
```

```

<400> 17
Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp
 1          5          10          15
Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser
 20          25          30
Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
 35          40          45
Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
 50          55          60
Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
 65          70          75
Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
 80          85          90
Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
 95          100          105
Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
 110          115          120
Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
 125          130          135
His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

```


Glu Ser Ser Asn	140	Ser Thr Asp Tyr Ile	145	Ala Met His Asp Val	150	Asp
	155		160		165	
Leu Leu Pro Leu	170	Asn Glu Glu Leu Asp	175	Tyr Gly Phe Pro Glu	180	Ala
	185		190		195	
Gly Pro Phe His	200	Val Ala Ser Pro Glu	205	Leu His Pro Leu Tyr	210	His
	215		220		225	
Tyr Arg Leu Cys	230	Asn Gly Met Ser Asn	235	Arg Phe Trp Gly Trp	240	Gly
	245		250		255	
Arg Glu Asp Asp	260	Glu Phe Tyr Arg Arg	265	Ile Lys Gly Ala Gly	270	Leu
	275		280		285	
Gln Leu Phe Arg	290	Pro Ser Gly Ile Thr	295	Thr Gly Tyr Lys Thr	300	Phe
	305		310		315	
Arg His Leu His	320	Asp Pro Ala Trp Arg	325	Lys Arg Asp Gln Lys		Arg
Ile Ala Ala Gln		Lys Gln Glu Gln Phe		Lys Val Asp Arg Glu		Gly
Gly Leu Asn Thr		Val Lys Tyr His Val		Ala Ser Arg Thr Ala		Leu
Ser Val Gly Gly		Ala Pro Cys Thr Val		Leu Asn Ile Met Leu		Asp
Cys Asp Lys Thr		Ala Thr Pro Trp Cys		Thr Phe Ser		

<210> 18
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 18
 gcgaacgctt cgaggagtcc tgg 23

<210> 19
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<223> Growth factor and cytokines receptors family.

<400> 22

```
Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Lys Gly
 1           5           10           15
Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
           20           25           30
Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
           35           40           45
Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
           50           55           60
Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
           65           70
```

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

```
gggacccatg cggccgtgac ccccggtctc ctagaggccc agcgcagccg 50
cagcggacaa aggagcatgt ccgcgccggg gaaggcccg cctccggccg 100
ccataaggct ccggtcgccg ctgggcccgc gccgcgctcc tgcccggccg 150
ggctccgggg cggcccgcta ggccagtgcg ccgccgctcg ccccgcaggc 200
cccgccccgc agcatggagc caccgggacg ccggcggggc cgcgcgagc 250
cgccgctgtt gctgccgctc tcgctgttag cgctgctcgc gctgctggga 300
ggcggcgggc gcggcgggcg cgcggcgctg cccgccggct gcaagcacga 350
tgggcggccc cgaggggctg gcagggcggc gggcgccgcc gagggcaagg 400
tggtgtgcag cagcctggaa ctgcgcgagg tcctgcccc agatactctg 450
cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500
gaagaatggc tcattttctg ggttaagtct ccttgaaaga ttggacctcc 550
gaaacaatct tattagtagt atagatccag gtgccttctg gggactgtca 600
tctctaaaaa gattggatct gacaaacaat cgaataggat gtctgaatgc 650
agacatattt cgaggactca ccaatctggt tcggctaaac ctttcgggga 700
atttgttttc ttcattatct caaggaactt ttgattatct tgcgtcatta 750
cggctcttgg aattccagac tgagtatctt ttgtgtgact gtaacatact 800
gtggatgcat cgctgggtaa aggagaagaa catcacgga cgggatacca 850
```

ggtgtgttta tctaagtca ctgcaggccc aaccagtcac aggcgtgaag 900
 caggagctgt tgacatgcga ccctccgctt gaattgccgt ctttctacat 950
 gactccatct catcgccaag ttgtgtttga aggagacagc cttcctttcc 1000
 agtgcattggc ttcatatatt gatcaggaca tgcaagtgtt gtggtatcag 1050
 gatgggagaa tagttgaaac cgatgaatcg caaggtatth ttgttgaaaa 1100
 gaacatgatt cacaactgct ccttgattgc aagtgcccta accatttcta 1150
 atattcaggc tggatctact ggaaattggg gctgtcatgt ccagacacaa 1200
 cgtgggaata atacgaggac tgtggatatt gtggtattag agagtctgc 1250
 acagtactgt cctccagaga ggggtgtaaa caacaaaggt gacttcagat 1300
 ggcccagaac attggcaggc attactgcat atctgcagtg tacgcggaac 1350
 acccatggca gtgggatata tcccggaaac ccacaggatg agagaaaagc 1400
 ttggcgcaga tgtgatagag gtggcttttg ggcagatgat gattattctc 1450
 gctgtcagta tgcaaatgat gtcactagag ttctttatat gtttaatcag 1500
 atgcccctca atcttaccaa tgccgtggca acagctcgac agttactggc 1550
 ttacactgtg gaagcagcca acttttctga caaatggat gttatatttg 1600
 tggcagaaat gattgaaaaa tttggaagat ttaccaagga ggaaaaatca 1650
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 tgatgaacgt gtcctgtggc tggcgcagag ggaagctaaa gcctgcagta 1750
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 gctcacgttt attcaacata ttcaccaat attgctctgg aagcttatgt 1850
 catcaagtct actggcttca cggggatgac ctgtaccgtg ttccagaaag 1900
 tggcagcctc tgatcgtaca ggactttcgg attatgggag gcgggatcca 1950
 gagggaaacc tggataagca gctgagcttt aagtgcaatg tttcaaatac 2000
 attttcgagt ctggcactaa aggtatgtta cattctgcaa tcatttaaga 2050
 ctatttacag ttaaattaga atgctccaaa tgttctgott cgcaaaataa 2100
 ccttattaaa agattttttt ttgcaggaag ataggtatta ttgcttttgc 2150
 tactgtttta aagaaaacta accaggaaga actgcattac gactttcaag 2200
 ggccctaggc atttttgcct ttgattccct ttcttcacat aaaaatatca 2250
 gaaattacat ttataactg cagtgggtata aatgcaaata tactattggt 2300

(Musical notation for Example 6)

```
<210> 24
<211> 616
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> sig_peptide
<222> 1-33
<223> Signal peptide.
```

```
<220>
<221> TRANSMEM
<222> 13-40
<223> Transmembrane domain (type II).
```

```

<400> 24
Met  Glu  Pro  Pro  Gly  Arg  Arg  Arg  Gly  Arg  Ala  Gln  Pro  Pro  Leu
   1                                10                      15

Leu  Leu  Pro  Leu  Ser  Leu  Leu  Ala  Leu  Leu  Ala  Leu  Leu  Gly  Gly
   20                                25                      30

Gly  Gly  Gly  Gly  Gly  Ala  Ala  Ala  Leu  Pro  Ala  Gly  Cys  Lys  His
   35                                40                      45

Asp  Gly  Arg  Pro  Arg  Gly  Ala  Gly  Arg  Ala  Ala  Gly  Ala  Ala  Glu
   50                                55                      60

Gly  Lys  Val  Val  Cys  Ser  Ser  Leu  Glu  Leu  Ala  Gln  Val  Leu  Pro
   65                                70                      75

Pro  Asp  Thr  Leu  Pro  Asn  Arg  Thr  Val  Thr  Leu  Ile  Leu  Ser  Asn
   80                                85                      90

```


380										385					390				
Gln	Asp	Glu	Arg	Lys	Ala	Trp	Arg	Arg	Cys	Asp	Arg	Gly	Gly	Phe					
				395					400					405					
Trp	Ala	Asp	Asp	Asp	Tyr	Ser	Arg	Cys	Gln	Tyr	Ala	Asn	Asp	Val					
				410					415					420					
Thr	Arg	Val	Leu	Tyr	Met	Phe	Asn	Gln	Met	Pro	Leu	Asn	Leu	Thr					
				425					430					435					
Asn	Ala	Val	Ala	Thr	Ala	Arg	Gln	Leu	Leu	Ala	Tyr	Thr	Val	Glu					
				440					445					450					
Ala	Ala	Asn	Phe	Ser	Asp	Lys	Met	Asp	Val	Ile	Phe	Val	Ala	Glu					
				455					460					465					
Met	Ile	Glu	Lys	Phe	Gly	Arg	Phe	Thr	Lys	Glu	Glu	Lys	Ser	Lys					
				470					475					480					
Glu	Leu	Gly	Asp	Val	Met	Val	Asp	Ile	Ala	Ser	Asn	Ile	Met	Leu					
				485					490					495					
Ala	Asp	Glu	Arg	Val	Leu	Trp	Leu	Ala	Gln	Arg	Glu	Ala	Lys	Ala					
				500					505					510					
Cys	Ser	Arg	Ile	Val	Gln	Cys	Leu	Gln	Arg	Ile	Ala	Thr	Tyr	Arg					
				515					520					525					
Leu	Ala	Gly	Gly	Ala	His	Val	Tyr	Ser	Thr	Tyr	Ser	Pro	Asn	Ile					
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Ala	Leu	Glu	Ala	Tyr	Val	Ile	Lys	Ser	Thr	Gly	Phe	Thr	Gly	Met					
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Thr	Cys	Thr	Val	Phe	Gln	Lys	Val	Ala	Ala	Ser	Asp	Arg	Thr	Gly					
				560					565					570					
Leu	Ser	Asp	Tyr	Gly	Arg	Arg	Asp	Pro	Glu	Gly	Asn	Leu	Asp	Lys					
				575					580					585					
Gln	Leu	Ser	Phe	Lys	Cys	Asn	Val	Ser	Asn	Thr	Phe	Ser	Ser	Leu					
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- <211> 24
- <212> DNA
- <213> Artificial
- <220>
- <221> Artificial Sequence
- <222> 1-24

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<211> 81
<212> PRT
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35 40 45
Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
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<212> PRT
<213> Homo sapiens
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				20					25					30
Ala	Leu	Thr	Gln	Pro	Leu	Gly	Leu	Leu	Arg	Leu	Leu	Gln	Leu	Val
				35					40					45
Ser	Thr	Cys	Val	Ala	Phe	Ser	Leu	Val	Ala	Ser	Val	Gly	Ala	Trp
				50					55					60
Thr	Gly	Ser	Met	Gly	Asn	Trp	Ser	Met	Phe	Thr	Trp	Cys	Phe	Cys
				65					70					75
Phe	Ser	Val	Thr	Leu	Ile	Ile	Leu	Ile	Val	Glu	Leu	Cys	Gly	Leu
				80					85					90
Gln	Ala	Arg	Phe	Pro	Leu	Ser	Trp	Arg	Asn	Phe	Pro	Ile	Thr	Phe
				95					100					105
Ala	Cys	Tyr	Ala	Ala	Leu	Phe	Cys	Leu	Ser	Ala	Ser	Ile	Ile	Tyr
				110					115					120
Pro	Thr	Thr	Tyr	Val	Gln	Phe	Leu	Ser	His	Gly	Arg	Ser	Arg	Asp
				125					130					135
His	Ala	Ile	Ala	Ala	Thr	Phe	Phe	Ser	Cys	Ile	Ala	Cys	Val	Ala
				140					145					150
Tyr	Ala	Thr	Glu	Val	Ala	Trp	Thr	Arg	Ala	Arg	Pro	Gly	Glu	Ile
				155					160					165
Thr	Gly	Tyr	Met	Ala	Thr	Val	Pro	Gly	Leu	Leu	Lys	Val	Leu	Glu
				170					175					180
Thr	Phe	Val	Ala	Cys	Ile	Ile	Phe	Ala	Phe	Ile	Ser	Asp	Pro	Asn
				185					190					195
Leu	Tyr	Gln	His	Gln	Pro	Ala	Leu	Glu	Trp	Cys	Val	Ala	Val	Tyr
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Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu
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Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu
230 235 240
Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu
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Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln
260 265 270
Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr
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Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr
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<213> Homo sapiens

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<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

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				20					25					30
Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
				35					40					45
His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
				50					55					60
Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
				65					70					75
Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
				80					85					90
Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
				95					100					105
Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
				110					115					120
Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg
				125					130					135
Phe	Ala	Ala	Gly	Val	Ala	Glu	Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys
				140					145					150
Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp
				155					160					165
Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala
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Gly	Gln	Leu	Pro	Leu	Gly	Pro	His	Leu	Gln	Asp	Leu	Phe	Thr	Gly
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His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu
				200					205					210
Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser
				215					220					225
Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu
				230					235					240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro
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 260 265 270
 Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser
 275 280 285
 Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu
 290 295 300
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 <213> Artificial

<220>
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 <222> 1-25
 <223> Synthetic construct

<400> 34
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<220>
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 <222> 1-50
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<220>
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 <222> 1-25
 <223> Synthetic construct.

<400> 36

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<212> DNA
<213> Artificial

<220>
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<223> Synthetic construct.

<400> 37
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<210> 38
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<400> 38
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<210> 39
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<210> 40
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<212> PRT
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35 40 45
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
50 55 60
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
65 70 75
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
80 85 90
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
95 100 105
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
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Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
125 130 135
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
140 145 150
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
155 160 165
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
170 175 180
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
185 190 195

Asp Ser Phe Thr Gly	200	Phè Thr Pro Tyr Gln Glu Lys Thr Thr Leu	205	210
Gln Pro Thr Leu Lys	215	Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn	220	225
Thr Ser Asp Pro Gln	230	Lys Glu Asn Arg Asn Thr Gly Ile Val Phe	235	240
Gly Ala Ile Leu Gly	245	Ala Ile Leu Gly Val Ser Leu Leu Thr Leu	250	255
Val Gly Tyr Leu Leu	260	Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser	265	270
His Arg Arg Leu Tyr	275	Asp Asp Arg Asn Glu Pro Val Leu Arg Leu	280	285
Asp Asn Ala Pro Glu	290	Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser	295	300
Tyr Tyr Asn Pro Thr	305	Leu Asn Asp Ser Ala Met Pro Glu Ser Glu	310	315
Glu Asn Ala Arg Asp	320	Gly Ile Pro Met Asp Asp Ile Pro Pro Leu	325	330

Arg Thr Ser Val

<210> 42
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<400> 42
 aacaggatct cctcttgacg tctgcagccc aggacgctga ttccagcagc 50
 gccttaccgc gcagcccga gattcactat ggtgaaaatc gccttcaata 100
 cccctaccgc cgtgcaaaag gaggaggcgc ggcaagacgt ggaggccctc 150
 ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200
 tgccacccag gaaaaagagg gctcctctgg gagatgtatg cttactctct 250
 taggcctttc attcatcttg gcaggactta ttgttggtgg agcctgcatt 300
 tacaagtact tcatgcccaa gagcaccatt taccgtggag agatgtgctt 350
 ttttgattct gaggatcctg caaattccct tcgtggagga gaggcctaact 400
 tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450
 atcattgatg tgctgtccc cagtttctct gatagtgacc ctgcagcaat 500
 tattcatgac ttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550

ggaactgcta tctgatgccc ctcaatactt ctattgttat gcctccaaaa 600
aatctggtag agctcttttg caaactggcg agtggcagat atctgcctca 650
aacttatgtg gttcgagaag acctagtgtc tgtggaggaa attcgtgatg 700
ttagtaacct tggcatcttt atttaccaac tttgcaataa cagaaagtcc 750
ttccgccttc gtgcgagaga cctcttgctg ggtttcaaca aacgtgccat 800
tgataaatgc tggaagatta gacacttccc caacgaattt attgttgaga 850
ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggtaata 900
agaagtcaga gatttacaat atgactttta cattaagggtt tatgggatac 950
tcaagatatatt tactcatgca ttactctat tgcttatgct ttaaaaaaag 1000
gaaaaaaaaa aaaactacta accactgcaa gctcttgtca aatttttagtt 1050
taattggcat tgcttggttt ttgaaactga aattacatga gtttcatttt 1100
ttctttgcat ttatagggtt tagatttctg aaagcagcat gaatatatca 1150
cctaacatcc tgacaataaa ttccatccgt tgtttttttt gtttgtttgt 1200
tttttctttt cctttaagta agctctttat tcatcttatg gtggagcaat 1250
tttaaaattt gaaatatttt aaattgtttt tgaacttttt gtgtaaaata 1300
tatcagatct caacattggt gggttctttt gtttttcatt ttgtacaact 1350
ttcttgaatt tagaaattac atctttgcag ttctgttagg tgctctgtaa 1400
ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450
aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaat 1500
tgtgtaggtg ctgaatgctg taaggagttt aggttgtagt aattctacaa 1550
ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43
<211> 263
<212> PRT
<213> Homo sapiens

<400> 43
Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu
1 5 10 15
Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg
20 25 30
Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
35 40 45
Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

50	55	60
Ser Phe Ile Leu Ala Gly Leu Ile Val	Gly Gly Ala Cys Ile Tyr	
65	70	75
Lys Tyr Phe Met Pro Lys Ser Thr Ile	Tyr Arg Gly Glu Met Cys	
80	85	90
Phe Phe Asp Ser Glu Asp Pro Ala Asn	Ser Leu Arg Gly Gly Glu	
95	100	105
Pro Asn Phe Leu Pro Val Thr Glu Glu	Ala Asp Ile Arg Glu Asp	
110	115	120
Asp Asn Ile Ala Ile Ile Asp Val Pro	Val Pro Ser Phe Ser Asp	
125	130	135
Ser Asp Pro Ala Ala Ile Ile His Asp	Phe Glu Lys Gly Met Thr	
140	145	150
Ala Tyr Leu Asp Leu Leu Leu Gly Asn	Cys Tyr Leu Met Pro Leu	
155	160	165
Asn Thr Ser Ile Val Met Pro Pro Lys	Asn Leu Val Glu Leu Phe	
170	175	180
Gly Lys Leu Ala Ser Gly Arg Tyr Leu	Pro Gln Thr Tyr Val Val	
185	190	195
Arg Glu Asp Leu Val Ala Val Glu Glu	Ile Arg Asp Val Ser Asn	
200	205	210
Leu Gly Ile Phe Ile Tyr Gln Leu Cys	Asn Asn Arg Lys Ser Phe	
215	220	225
Arg Leu Arg Arg Arg Asp Leu Leu Leu	Gly Phe Asn Lys Arg Ala	
230	235	240
Ile Asp Lys Cys Trp Lys Ile Arg His	Phe Pro Asn Glu Phe Ile	
245	250	255
Val Glu Thr Lys Ile Cys Gln Glu		
260		

<210> 44
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 44
 gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-20
<223> Synthetic construct.

<400> 45
gggaactgct atctgatgcc 20

<210> 46
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 46
caggatctcc tcttgagtc tgcagc 26

<210> 47
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-28
<223> Synthetic construct.

<400> 47
cttctcgaac cacataagtt tgaggcag 28

<210> 48
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 48
cacgattccc tccacagcaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

<400> 49
ggaggaggga gggcgggcag gcgccagccc agagcagccc cgggcaccag 50

cacggactct ctcttccagc ccagggtgcc cccactctcg ctccattcgg 100
 cgggagcacc cagtcctgta cgccaaggaa ctggtcctgg gggcaccatg 150
 gtttcggcgg cagccccag cctcctcacc cttctgttgc tgctgctggg 200
 gtctgtgcct gctaccgacg cccgctctgt gccctgaag gccacgttcc 250
 tggaggatgt ggcgggtagt ggggaggccg agggctcgtc ggcctcctcc 300
 ccgagcctcc cgccaccctg gaccccggcc ctacgcccc catcgatggg 350
 gccccagccc acaaccctgg gggggccatc acccccacc aacttcctgg 400
 atgggatagt ggacttcttc cgccagtacg tgatgctgat tgctgtggtg 450
 ggctccctgg cttttctgct gatgttcacg gtctgtgccg cggtcacac 500
 ccggcagaag cagaaggcct cggcctatta cccatcgacc ttccccaaga 550
 agaagtacgt ggaccagagt gaccgggccc ggggcccccg ggccttcagt 600
 gaggtccccg acagagcccc cgacagcagg cccgaggaag ccctggattc 650
 ctcccggcag ctccaggccg acatcttggc cgccaccag aacctcaagt 700
 cccccaccag ggctgcactg ggcgggtggg acggagccag gatggtggag 750
 ggcaggggag cagaggaaga ggagaagggc agccaggagg gggaccagga 800
 agtccaggga catggggtcc cagtggagac accagaggcg caggaggagc 850
 cgtgctcagg ggtccttgag ggggctgtgg tggccggtga gggccaaggg 900
 gagctggaag ggtctctctt gttagcccag gaagcccagg gaccagtggg 950
 tcccccgaa agcccctgtg cttgcagcag tgtccacccc agtgtctaac 1000
 agtctcccg ggctgccagc cctgactgtc gggcccccaa gtggtcacct 1050
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 cttggcctcc ctgtggtgcc aatcccagca tgtgctgatt ctacagcagg 1150
 cagaaatgct ggtccccggt gccccggagg aatcttacca agtgccatca 1200
 tccttcacct cagcagcccc aaagggtac atctacagc acagctcccc 1250
 tgacaaagtg agggagggca cgtgtccctg tgacagccag gataaaacat 1300
 cccccaaagt gctgggatta caggcgtgag ccaccgtgcc cggcccaaac 1350
 tactttttta aacagctaca gggtaaaatc ctgcagcacc cactctggaa 1400
 aatactgctc ttaattttcc tgaagggtgg ccctgtttc tagttggtcc 1450
 aggattaggg atgtggggta tagggcattt aaatcctctc aagcgtctc 1500

caagcacccc cggcctgggg gtgagtttct catcccgcta ctgctgctgg 1550
gatcagggttg aatgaatgga actcttctctg tctggcctcc aaagcagcct 1600
agaagctgag gggctgtgtt tgaggggacc tccaccctgg ggaagtccga 1650
ggggctgggg aagggtttct gacgcccagc ctggagcagg ggggccctgg 1700
ccacccctctg ttgctcacac attgtctggc agcctgtgtc cacaatattc 1750
gtcagtcctc gacagggagc ctgggctccg tcctgcttta gggaggctct 1800
ggcaggaggt cctctcccc atccctccat ctggggctcc cccaacctct 1850
gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900
attccggcct gaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1950
aaaaaaaaa aaaaaaaga 1969

<210> 50
<211> 283
<212> PRT
<213> Homo sapiens

<400> 50
Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu
1 5 10 15
Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu
20 25 30
Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
35 40 45
Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
50 55 60
Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
65 70 75
Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe
80 85 90
Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala
95 100 105
Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln
110 115 120
Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys
125 130 135
Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe
140 145 150
Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala
155 160 165

Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr
				170					175					180
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp
				185					190					195
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys
				200					205					210
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro
				215					220					225
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu
				230					235					240
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly
				245					250					255
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro
				260					265					270
Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val		
				275					280					

<210> 51
 <211> 1734
 <212> DNA
 <213> Homo sapiens

<400> 51
 gtggactctg agaagcccag gcagttgagg acaggagaga gaaggctgca 50
 gaccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100
 gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga 150
 agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc 200
 cctggcctgc ctctgctgg ccctctgcct gggcagtgagg gaggtggcc 250
 ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300
 ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggccattgg 350
 caaagaggcc ggaggggag ctggctctaa agtcagttag gcccttggcc 400
 aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt 450
 ggcgcagcag atgctttggg caacagggtc ggggaagcag cccatgctct 500
 gggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550
 acggagcaga tgctgtccgc ggctcctggc aggggggtgcc tggccacagt 600
 ggtgcttggg aaacttctgg aggccatggc atctttggct ctcaaggtgg 650
 ccttggaggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700

tccacggata ccccggaac tcagcaggca gctttggaat gaatcctcag 750
 ggagctccct ggggtcaagg aggcaatgga gggccaccaa actttgggac 800
 caaactcag ggagctgtgg ccagcctgg ctatggttca gtgagagcca 850
 gcaaccagaa tgaaggtgc acgaatcccc caccatctgg ctgaggtgga 900
 ggctccagca actctggggg aggcagcggc tcacagtcgg gcagcagtg 950
 cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000
 gcagtggcag cagcagtggc agcagcagtg gcggcagcag tggcggcagc 1050
 agtgggtggca gcagtggcaa cagtgggtggc agcagaggtg acagcggcag 1100
 tgagtccctc tggggatcca gcaccggctc ctctccggc aaccacggtg 1150
 ggagcggcgg aggaaatgga cataaacccg ggtgtgaaaa gccagggaat 1200
 gaagcccgcg ggagcgggga atctgggatt cagggttca gaggacagg 1250
 agtttccagc aacatgaggg aaataagcaa agagggcaat cgctccttg 1300
 gaggtctctg agacaattat cgggggcaag ggtcgagctg gggcagtgga 1350
 ggaggtgacg ctgttggtgg agtcaatact gtgaactctg agacgtctcc 1400
 tgggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450
 gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcatc 1500
 ccgtgacctc cagacaagga gccaccagat tggatgggag cccccacact 1550
 ccctccttaa aacaccaccc tctcatcact aatctcagcc cttgcccttg 1600
 aaataaacct tagctgcccc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 52
 <211> 440
 <212> PRT
 <213> Homo sapiens

<400> 52
 Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys
 1 5 10 15
 Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser
 20 25 30
 Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
 35 40 45
 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

50										55					60				
Gly	Ala	Ala	Gly	Ser	Lys	Val	Ser	Glu	Ala	Leu	Gly	Gln	Gly	Thr					
				65					70					75					
Arg	Glu	Ala	Val	Gly	Thr	Gly	Val	Arg	Gln	Val	Pro	Gly	Phe	Gly					
				80					85					90					
Ala	Ala	Asp	Ala	Leu	Gly	Asn	Arg	Val	Gly	Glu	Ala	Ala	His	Ala					
				95					100					105					
Leu	Gly	Asn	Thr	Gly	His	Glu	Ile	Gly	Arg	Gln	Ala	Glu	Asp	Val					
				110					115					120					
Ile	Arg	His	Gly	Ala	Asp	Ala	Val	Arg	Gly	Ser	Trp	Gln	Gly	Val					
				125					130					135					
Pro	Gly	His	Ser	Gly	Ala	Trp	Glu	Thr	Ser	Gly	Gly	His	Gly	Ile					
				140					145					150					
Phe	Gly	Ser	Gln	Gly	Gly	Leu	Gly	Gly	Gln	Gly	Gln	Gly	Asn	Pro					
				155					160					165					
Gly	Gly	Leu	Gly	Thr	Pro	Trp	Val	His	Gly	Tyr	Pro	Gly	Asn	Ser					
				170					175					180					
Ala	Gly	Ser	Phe	Gly	Met	Asn	Pro	Gln	Gly	Ala	Pro	Trp	Gly	Gln					
				185					190					195					
Gly	Gly	Asn	Gly	Gly	Pro	Pro	Asn	Phe	Gly	Thr	Asn	Thr	Gln	Gly					
				200					205					210					
Ala	Val	Ala	Gln	Pro	Gly	Tyr	Gly	Ser	Val	Arg	Ala	Ser	Asn	Gln					
				215					220					225					
Asn	Glu	Gly	Cys	Thr	Asn	Pro	Pro	Pro	Ser	Gly	Ser	Gly	Gly	Gly					
				230					235					240					
Ser	Ser	Asn	Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gln	Ser	Gly	Ser	Ser					
				245					250					255					
Gly	Ser	Gly	Ser	Asn	Gly	Asp	Asn	Asn	Asn	Gly	Ser	Ser	Ser	Gly					
				260					265					270					
Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Gly	Ser					
				275					280					285					
Ser	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ser	Gly	Asn	Ser	Gly	Gly	Ser					
				290					295					300					
Arg	Gly	Asp	Ser	Gly	Ser	Glu	Ser	Ser	Trp	Gly	Ser	Ser	Thr	Gly					
				305					310					315					
Ser	Ser	Ser	Gly	Asn	His	Gly	Gly	Ser	Gly	Gly	Gly	Asn	Gly	His					
				320					325					330					
Lys	Pro	Gly	Cys	Glu	Lys	Pro	Gly	Asn	Glu	Ala	Arg	Gly	Ser	Gly					
				335					340					345					

Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn
350 355 360
Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser
365 370 375
Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly
380 385 390
Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser
395 400 405
Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser
410 415 420
Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg
425 430 435
Ser Ser Arg Ile Pro
440

<210> 53
<211> 3580
<212> DNA
<213> Homo sapiens

<400> 53
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ctttgctgac catgttggtc ccttgctgga atattaccgg gacatcttca 150
ctctcctgct gcgcctgcac cggagcttgg tgttgctgca ggagagttag 200
gggaagatgt gtttcctgaa caagctgctg ctacttgctg tcctgggctg 250
gcttttccag attccacag tccctgagga cttgttcttt ctggaagagg 300
gtccctcata tgcctttgag gtggacacag tagccccaga gcatggcttg 350
gacaatgcgc ctgtggtgga ccagcagctg ctctacacct gctgccccta 400
catcggagag ctccggaac tgctcgcttc gtgggtgtca ggcagtagtg 450
gacggagtgg gggcttcatg aggaaaatca cccccaccac taccaccagc 500
ctgggagccc agccttccca gaccagccag gggctgcagg cacagctcgc 550
ccaggccttt ttccacaacc agccgccctc cttgcgccgg accgtagagt 600
tcgtggcaga aagaattgga tcaaactgtg tcaaacatat caaggctaca 650
ctggtggcag atctggtgcg ccaggcagag tcaacttctcc aagagcagct 700
ggtgacacag ggagaggaag ggggagaccc agcccagctg ttggagatct 750
tgtgttccca gctgtgccct cacggggccc aggcattggc cctggggcgg 800

gagttctgtc aaaggaagag ccctggggct gtgcggggcgc tgcttcacaga 850
ggagaccccg gcagccgttc tgagcagtgc agagaacatt gctgtggggc 900
ttgcaacaga gaaagcctgt gcttggtgtg cagccaacat cacagcactg 950
atcaggaggg aggtgaaagc agcagtgagt cgcacacttc gagcccaggg 1000
tcctgaacct gctgcccggg gggagcggag gggctgctcc cgcgcctgac 1050
gtgctctcct tggcctgagg gccacgggac cctgacgagg gagtctcccc 1100
agagcatctg gaacagctcc taggccagct gggccagacg ctgcggtgcc 1150
gccagttcct gtgcccacct gctgagcagc atctggcaaa gtgctctgtg 1200
gagttagctt ccctcctcgt tgcagatcaa attcctatcc tagggccccc 1250
ggcacagtac aggtctggaga gagggcaggc tcgaaggctt ctgcacatgc 1300
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ctgctgagcc caagaaatgt ggggcttctg gcagacacaa ggccaaggga 1400
gtgggacttg ctgctattct tgctacggga gctggtggag aagggtctga 1450
tgggacggat ggagatagag gcctgcctgg gcagcctcca ccaggcccag 1500
tggccagggg actttgctga agaattagca acactgtcta atctgtttct 1550
agccgagccc cacctgccag aaccccagct aagagcctgt gagttggtgc 1600
agccaaaccg gggcactgtg ctggcccaga gctagggctg agaagtggcc 1650
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ccaagtgcc aatgcagacc ctactggtt ggggtgtagc tgggtctaca 1750
gtcagacttc ctgctctaag ggtgtcactg cctggcatcc caccacgcga 1800
atcctagagg aaggagagtt ggcctgattt gggattatgg cagaaaagtc 1850
cagagatgcc agtcctggag tagaagaggt ggtgtttgtt tatctcttgg 1900
atactaaatg aaatgagggt tgtgggcttg tcaacacaga attcaagcct 1950
catttgctat ccagcatct cttaaaactt tgtagtcttg gaattcatga 2000
cagaggcaaa tgactcctgc ttaacttatg aagaaagtta aaacatgaat 2050
cttgggagtc tacattttct tatcaccagg agctggactg ccatctcctt 2100
ataaatgcct aacacaggcc gggctctggtg gctcatgctt gtaatcccag 2150
cactttgaga ggctgagggt cggcggactg cctgagggtca ggaattcaag 2200
accagcctgg ccaacatggc aaaaccccat ctctactaaa aataaaaaaa 2250

ttattagctg ggcattggtg tgtgtgcctg taatcccagc tactcaggag 2300
gatgaggcag gagacctgct tgaacctgga ggtggagggt gcagttagcc 2350
gaggtcgcac cactgcactc cagtctgggt aacagagcga gacttttctag 2400
aaaaagccta acaaacagat aaggtaggac tcaaccaact gaaacctgac 2450
tttccccctg taccttcagc cctgtgacg gtagtaacct cttgagacct 2500
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ctgggttttct ttaaaaaaaaa aaaaaaaaaa agggcgcccg cccttttttt 2600
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ttttattaaa attctcccca cacgatggct cctgcaatct gccacagctc 2700
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<212> PRT
<213> Homo sapiens

<400> 54
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 Glu Gly Pro Ser Tyr Ala Phe Glu Val Asp Thr Val Ala Pro Glu
 35 40 45
 His Gly Leu Asp Asn Ala Pro Val Val Asp Gln Gln Leu Leu Tyr
 50 55 60
 Thr Cys Cys Pro Tyr Ile Gly Glu Leu Arg Lys Leu Leu Ala Ser
 65 70 75
 Trp Val Ser Gly Ser Ser Gly Arg Ser Gly Gly Phe Met Arg Lys
 80 85 90
 Ile Thr Pro Thr Thr Thr Thr Ser Leu Gly Ala Gln Pro Ser Gln
 95 100 105
 Thr Ser Gln Gly Leu Gln Ala Gln Leu Ala Gln Ala Phe Phe His
 110 115 120
 Asn Gln Pro Pro Ser Leu Arg Arg Thr Val Glu Phe Val Ala Glu
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 Arg Ile Gly Ser Asn Cys Val Lys His Ile Lys Ala Thr Leu Val
 140 145 150
 Ala Asp Leu Val Arg Gln Ala Glu Ser Leu Leu Gln Glu Gln Leu
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 Val Thr Gln Gly Glu Glu Gly Gly Asp Pro Ala Gln Leu Leu Glu
 170 175 180
 Ile Leu Cys Ser Gln Leu Cys Pro His Gly Ala Gln Ala Leu Ala
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 Leu Gly Arg Glu Phe Cys Gln Arg Lys Ser Pro Gly Ala Val Arg
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 Ala Leu Leu Pro Glu Glu Thr Pro Ala Ala Val Leu Ser Ser Ala
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 Glu Asn Ile Ala Val Gly Leu Ala Thr Glu Lys Ala Cys Ala Trp
 230 235 240
 Leu Ser Ala Asn Ile Thr Ala Leu Ile Arg Arg Glu Val Lys Ala
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<210> 55
 <211> 2401
 <212> DNA
 <213> Homo sapiens

<400> 55
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<210> 56
<211> 299
<212> PRT
<213> Homo sapiens

<400> 56
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Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro	
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Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro	
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Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg	
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Arg	Leu	Gln	Arg	Met	Pro	Tyr	His	Tyr	Tyr	Glu	Pro	Lys	Gly	Pro	
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Asn	His	His	Arg	Phe	Ile	Thr	Glu	Lys	Arg	Val	Phe	Ser	Ser	Trp	
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 <211> 4277
 <212> DNA
 <213> Homo sapiens

<400> 57

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<210> 58

<211> 1115

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305 310 315

Asn Val Gln Val Phe Glu Pro Pro Glu Val Thr Met Glu Leu Ser
320 325 330

Gln Leu Val Ile Pro Trp Gly Gln Ser Ala Lys Leu Thr Cys Glu
335 340 345

Val Arg Gly Asn Pro Pro Pro Ser Val Leu Trp Leu Arg Asn Ala
350 355 360

Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala
365 370 375

Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln
380 385 390

Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln
395 400 405

Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp
410 415 420

Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu
425 430 435

Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg
440 445 450

Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu
455 460 465

Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser
470 475 480

Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro
485 490 495

Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val
500 505 510

Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile
515 520 525

Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu
530 535 540

Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys
545 550 555

Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg

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Arg	Asp	Asp	Pro	Gly 590	Ala	Ser	Pro	Gln		Ser 595	Ser	Ser	Gln	Pro	Asp 600
His	Gly	Arg	Leu	Ser 605	Pro	Pro	Glu	Ala		Pro 610	Asp	Arg	Pro	Thr	Ile 615
Ser	Thr	Ala	Ser	Glu 620	Thr	Ser	Val	Tyr		Val 625	Thr	Trp	Ile	Pro	Arg 630
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Lys	Leu	Lys	Lys	Val 650	Gly	Asp	Trp	Ile		Leu 655	Ala	Thr	Ser	Ala	Ile 660
Pro	Pro	Ser	Arg	Leu 665	Ser	Val	Glu	Ile		Thr 670	Gly	Leu	Glu	Lys	Gly 675
Thr	Ser	Tyr	Lys	Phe 680	Arg	Val	Arg	Ala		Leu 685	Asn	Met	Leu	Gly	Glu 690
Ser	Glu	Pro	Ser	Ala 695	Pro	Ser	Arg	Pro		Tyr 700	Val	Val	Ser	Gly	Tyr 705
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Phe	Thr	Asp	Ala	Val 725	Asn	Glu	Thr	Thr		Ile 730	Met	Leu	Lys	Trp	Met 735
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Lys	Ala	Arg	Lys	Ser 815	Ser	Gly	Gln	Pro		Gly 820	Arg	Leu	Pro	Pro	Pro 825
Thr	Leu	Ala	Pro	Pro 830	Gln	Pro	Pro	Leu		Pro 835	Glu	Thr	Ile	Glu	Arg 840
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 <223> Synthetic construct.

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 <210> 60
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 60
 gcacacgtag cctgtcgctg gagc 24

 <210> 61
 <211> 42
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-42
 <223> Synthetic construct.

 <400> 61
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 <210> 62
 <211> 1661
 <212> DNA
 <213> Homo sapiens

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 <221> unsure
 <222> 678
 <223> unknown base

 <400> 62
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<211> 487
<212> PRT
<213> Homo sapiens

<220>
 <221> unsure
 <222> 196, 386
 <223> unknown amino acid

<400> 63

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Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	20	25	30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	35	40	45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	50	55	60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	65	70	75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	80	85	90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	95	100	105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	110	115	120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	125	130	135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	140	145	150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	155	160	165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	170	175	180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	185	190	195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	200	205	210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	215	220	225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	230	235	240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	245	250	255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala				

				260					265					270
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Val	Ile	Phe	Ser	His 290	Ser	Ala	Ala	Arg	Ala 295	Val	Cys	Asp	Asn	Leu 300
Leu	Asn	Val	Pro	Asp 305	Asp	Ile	Leu	Gln	Leu 310	Leu	Lys	Asn	Gly	Gly 315
Ile	Val	Met	Val	Thr 320	Leu	Ser	Met	Gly	Val 325	Leu	Gln	Cys	Asn	Leu 330
Leu	Ala	Asn	Val	Ser 335	Thr	Val	Ala	Asp	His 340	Phe	Asp	His	Ile	Arg 345
Ala	Val	Ile	Gly	Ser 350	Glu	Phe	Ile	Gly	Ile 355	Gly	Gly	Asn	Tyr	Asp 360
Gly	Thr	Gly	Arg	Phe 365	Pro	Gln	Gly	Leu	Glu 370	Asp	Val	Ser	Thr	Tyr 375
Pro	Val	Leu	Ile	Glu 380	Glu	Leu	Leu	Ser	Arg 385	Xaa	Trp	Ser	Glu	Glu 390
Glu	Leu	Gln	Gly	Val 395	Leu	Arg	Gly	Asn	Leu 400	Leu	Arg	Val	Phe	Arg 405
Gln	Val	Glu	Lys	Val 410	Arg	Glu	Glu	Ser	Arg 415	Ala	Gln	Ser	Pro	Val 420
Glu	Ala	Glu	Phe	Pro 425	Tyr	Gly	Gln	Leu	Ser 430	Thr	Ser	Cys	His	Ser 435
His	Leu	Val	Pro	Gln 440	Asn	Gly	His	Gln	Ala 445	Thr	His	Leu	Glu	Val 450
Thr	Lys	Gln	Pro	Thr 455	Asn	Arg	Val	Pro	Trp 460	Arg	Ser	Ser	Asn	Ala 465
Ser	Pro	Tyr	Leu	Val 470	Pro	Gly	Leu	Val	Ala 475	Ala	Ala	Thr	Ile	Pro 480
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<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 64
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<210> 65
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 65
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<210> 66
 <211> 47
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-47
 <223> Synthetic construct.

<400> 66
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<210> 67
 <211> 1564
 <212> DNA
 <213> Homo sapiens

<400> 67
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 ggcccagcaa gcctgataag catgaagctc ttatcttttg tggtgtggt 150
 cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200
 tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250
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<210> 68
<211> 183
<212> PRT
<213> Homo sapiens

<400> 68
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Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
35 40 45
Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
50 55 60

Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu
65 70 75
Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val
80 85 90
Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr
95 100 105
Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp
110 115 120
Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala
125 130 135
Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
140 145 150
Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys
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Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys
170 175 180
Met Leu Ser

<210> 69
<211> 3170
<212> DNA
<213> Homo sapiens

<400> 69
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tcgccgggag atggccgcgt tgatgcggag caaggattcg tcctgctgcc 250
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<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

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Leu	Leu	Ala	Ala	Val	Leu	Met	Val	Glu	Ser	Ser	Gln	Ile	Gly	Ser
				20					25					30
Ser	Arg	Ala	Lys	Leu	Asn	Ser	Ile	Lys	Ser	Ser	Leu	Gly	Gly	Glu
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<210> 71
<211> 1809
<212> DNA
<213> Homo sapiens
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acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150
cttcccttta acttcttatg tcagaatgag gaaggatagc tqcatttatt 200
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tagtcagttt tcattgcata gtaatatatt catgtagtat tttctaagtt 250
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Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser
				275					280					285
Ser	Ser	Tyr	Asp	Gln	Ser	Ser	Val	His	Asn	Arg	Ile	Pro	Tyr	Gln
				290					295					300
Ser	Pro	Val	Ser	Ser	Ser	Glu	Ser	Ala	Pro	Gly	Thr	Ile	Met	Asn
				305					310					315
Gly	His	Gly	Gly	Gly	Arg	Ser	Gln	Gln	Thr	Leu	Asp	Ser	Lys	Tyr
				320					325					330
Ser	Ser	Lys	Leu	Leu	Leu	Ser	Trp	Leu	Val	Pro	Thr	Lys	Gln	Arg
				335					340					345
Lys	Arg	Ile	Ala	His	Val	Met	Trp	Lys	Thr	Pro	Val	Gly	Gln	Trp
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Leu Ile Arg

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.

 <400> 73
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 <210> 74
 <211> 22
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 <213> Artificial

 <220>
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 <222> 1-22
 <223> Synthetic construct.

 <400> 74
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 <210> 75
 <211> 50

<212> DNA
<213> Artificial

<220>
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<222> 1-50
<223> Synthetic construct

<400> 75
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<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
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<210> 77
<211> 341
<212> PRT
<213> Homo sapiens

<400> 77
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Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu
35 40 45
Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro
50 55 60
Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val
65 70 75

Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His	80	85	90
Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His	95	100	105
Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg	110	115	120
Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro	125	130	135
Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu	140	145	150
Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp	155	160	165
Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu	170	175	180
His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala	185	190	195
Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser	200	205	210
Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val	215	220	225
Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln	230	235	240
Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu	245	250	255
Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu	260	265	270
Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn	275	280	285
Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg	290	295	300
Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu	305	310	315
Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp	320	325	330
Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys	335	340	

<210> 78
 <211> 2243
 <212> DNA
 <213> Homo sapiens

<400> 78

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Tyr Leu Ala Val Ala Ser Thr Val Pro Ser Met Leu Cys Leu Val
110 115 120

Ala Asn Phe Leu Leu Val Asn Arg Val Ala Val His Ile Arg Val
125 130 135

Leu Ala Ser Leu Thr Val Ile Leu Ala Ile Phe Met Val Ile Thr
140 145 150

Ala Leu Val Lys Val Asp Thr Ser Ser Trp Thr Arg Gly Phe Phe
155 160 165

Ala Val Thr Ile Val Cys Met Val Ile Leu Ser Gly Ala Ser Thr
170 175 180

Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser Phe Pro Met
185 190 195

Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly Gly Thr
200 205 210

Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser Asp
215 220 225

Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe
230 235 240

Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu
245 250 255

Tyr Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe
260 265 270

Ser Gly Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser
275 280 285

Val Ala Ser Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro
290 295 300

Ile Leu Lys Lys Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val
305 310 315

Phe Phe Ile Thr Ser Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile
320 325 330

Glu Ser Leu Asn Lys Gly Ser Gly Ser Leu Trp Thr Thr Lys Phe
335 340 345

Phe Ile Pro Leu Thr Thr Phe Leu Leu Tyr Asn Phe Ala Asp Leu
350 355 360

Cys Gly Arg Gln Leu Thr Ala Trp Ile Gln Val Pro Gly Pro Asn
365 370 375

Ser Lys Ala Leu Pro Gly Phe Val Leu Leu Arg Thr Cys Leu Ile
380 385 390

Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro Arg Val His Leu Lys

	395	400	405
Thr Val Val Phe Gln Ser Asp Val Tyr	Pro Ala Leu Leu Ser Ser		
410	415	420	
Leu Leu Gly Leu Ser Asn Gly Tyr Leu	Ser Thr Leu Ala Leu Leu		
425	430	435	
Tyr Gly Pro Lys Ile Val Pro Arg Glu	Leu Ala Glu Ala Thr Gly		
440	445	450	
Val Val Met Ser Phe Tyr Val Cys Leu	Gly Leu Thr Leu Gly Ser		
455	460	465	
Ala Cys Ser Thr Leu Leu Val His Leu	Ile		
470	475		

<210> 80
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 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 80
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<210> 81
 <211> 23
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Artificial sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 81
 cgtagtgac acagaagccc agg 23

<210> 82
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-49
 <223> Synthetic construct.

<400> 82
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<210> 83
 <211> 1844

<212> DNA

<213> Homo sapiens

<400> 83

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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84
 <211> 567
 <212> PRT
 <213> Homo sapiens

<400> 84
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 35 40 45
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln
 50 55 60
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala
 65 70 75
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala
 80 85 90
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn
 95 100 105
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser
 110 115 120
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu
 125 130 135
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His
 140 145 150
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys
 155 160 165

Leu Gly Tyr Ala	Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu	170	175	180
Asp Ile Tyr Gln	Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys	185	190	195
Ala Leu Gly Cys	Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr	200	205	210
Leu Leu Glu Tyr	Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala	215	220	225
Val Gln Leu Leu	Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr	230	235	240
Leu Ser Phe Ala	Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp	245	250	255
Arg Leu Gln Tyr	Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro	260	265	270
Arg Ala Leu Leu	Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala	275	280	285
Pro Val Val Ala	Met Thr Gln Gly Pro His Asp Val His Val Gln	290	295	300
Ile Glu Thr Ser	Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala	305	310	315
Asp Val Val Leu	Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile	320	325	330
Thr Phe Ser Pro	Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg	335	340	345
Arg Leu His Tyr	Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg	350	355	360
Arg Pro Phe Trp	Arg Glu Glu His Ile Glu Gly Gly His Ser Asn	365	370	375
Thr Asp Arg Pro	Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu	380	385	390
Gly Ala Leu Leu	Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala	395	400	405
Ala Phe Ala Gly	Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu	410	415	420
Asp Asp Val Ala	Ala Leu His Gly Pro Val Val Arg Gln Leu Trp	425	430	435
Asp Gly Thr Gly	Val Val Lys Arg Trp Ala Glu Asp Gln His Ser	440	445	450
Gln Gly Gly Phe	Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu			

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<210> 86
 <211> 739
 <212> PRT
 <213> Homo sapiens

<400> 86
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 Gly Lys Lys Asp Arg Asp Ser Cys Gly Arg Lys Asn Ser Glu Pro
 20 25 30

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Gln	Gly	Leu	Asn	Phe 50	Leu	Leu	Leu	Phe	Thr 55	Lys	Met	Leu	Phe	Ile 60
Phe	Asn	Phe	Leu	Phe 65	Ser	Pro	Leu	Pro	Thr 70	Pro	Ala	Leu	Ile	Cys 75
Ile	Leu	Thr	Phe	Gly 80	Ala	Ala	Ile	Phe	Leu 85	Trp	Leu	Ile	Thr	Arg 90
Pro	Gln	Pro	Val	Leu 95	Pro	Leu	Leu	Asp	Leu 100	Asn	Asn	Gln	Ser	Val 105
Gly	Ile	Glu	Gly	Gly 110	Ala	Arg	Lys	Gly	Val 115	Ser	Gln	Lys	Asn	Asn 120
Asp	Leu	Thr	Ser	Cys 125	Cys	Phe	Ser	Asp	Ala 130	Lys	Thr	Met	Tyr	Glu 135
Val	Phe	Gln	Arg	Gly 140	Leu	Ala	Val	Ser	Asp 145	Asn	Gly	Pro	Cys	Leu 150
Gly	Tyr	Arg	Lys	Pro 155	Asn	Gln	Pro	Tyr	Arg 160	Trp	Leu	Ser	Tyr	Lys 165
Gln	Val	Ser	Asp	Arg 170	Ala	Glu	Tyr	Leu	Gly 175	Ser	Cys	Leu	Leu	His 180
Lys	Gly	Tyr	Lys	Ser 185	Ser	Pro	Asp	Gln	Phe 190	Val	Gly	Ile	Phe	Ala 195
Gln	Asn	Arg	Pro	Glu 200	Trp	Ile	Ile	Ser	Glu 205	Leu	Ala	Cys	Tyr	Thr 210
Tyr	Ser	Met	Val	Ala 215	Val	Pro	Leu	Tyr	Asp 220	Thr	Leu	Gly	Pro	Glu 225
Ala	Ile	Val	His	Ile 230	Val	Asn	Lys	Ala	Asp 235	Ile	Ala	Met	Val	Ile 240
Cys	Asp	Thr	Pro	Gln 245	Lys	Ala	Leu	Val	Leu 250	Ile	Gly	Asn	Val	Glu 255
Lys	Gly	Phe	Thr	Pro 260	Ser	Leu	Lys	Val	Ile 265	Ile	Leu	Met	Asp	Pro 270
Phe	Asp	Asp	Asp	Leu 275	Lys	Gln	Arg	Gly	Glu 280	Lys	Ser	Gly	Ile	Glu 285
Ile	Leu	Ser	Leu	Tyr 290	Asp	Ala	Glu	Asn	Leu 295	Gly	Lys	Glu	His	Phe 300
Arg	Lys	Pro	Val	Pro 305	Pro	Ser	Pro	Glu	Asp 310	Leu	Ser	Val	Ile	Cys 315
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr

				320					325					330
His	Gln	Asn	Ile	Val 335	Ser	Asn	Ala	Ala	Ala 340	Phe	Leu	Lys	Cys	Val 345
Glu	His	Ala	Tyr	Glu 350	Pro	Thr	Pro	Asp	Asp 355	Val	Ala	Ile	Ser	Tyr 360
Leu	Pro	Leu	Ala	His 365	Met	Phe	Glu	Arg	Ile 370	Val	Gln	Ala	Val	Val 375
Tyr	Ser	Cys	Gly	Ala 380	Arg	Val	Gly	Phe	Phe 385	Gln	Gly	Asp	Ile	Arg 390
Leu	Leu	Ala	Asp	Asp 395	Met	Lys	Thr	Leu	Lys 400	Pro	Thr	Leu	Phe	Pro 405
Ala	Val	Pro	Arg	Leu 410	Leu	Asn	Arg	Ile	Tyr 415	Asp	Lys	Val	Gln	Asn 420
Glu	Ala	Lys	Thr	Pro 425	Leu	Lys	Lys	Phe	Leu 430	Leu	Lys	Leu	Ala	Val 435
Ser	Ser	Lys	Phe	Lys 440	Glu	Leu	Gln	Lys	Gly 445	Ile	Ile	Arg	His	Asp 450
Ser	Phe	Trp	Asp	Lys 455	Leu	Ile	Phe	Ala	Lys 460	Ile	Gln	Asp	Ser	Leu 465
Gly	Gly	Arg	Val	Arg 470	Val	Ile	Val	Thr	Gly 475	Ala	Ala	Pro	Met	Ser 480
Thr	Ser	Val	Met	Thr 485	Phe	Phe	Arg	Ala	Ala 490	Met	Gly	Cys	Gln	Val 495
Tyr	Glu	Ala	Tyr	Gly 500	Gln	Thr	Glu	Cys	Thr 505	Gly	Gly	Cys	Thr	Phe 510
Thr	Leu	Pro	Gly	Asp 515	Trp	Thr	Ser	Gly	His 520	Val	Gly	Val	Pro	Leu 525
Ala	Cys	Asn	Tyr	Val 530	Lys	Leu	Glu	Asp	Val 535	Ala	Asp	Met	Asn	Tyr 540
Phe	Thr	Val	Asn	Asn 545	Glu	Gly	Glu	Val	Cys 550	Ile	Lys	Gly	Thr	Asn 555
Val	Phe	Lys	Gly	Tyr 560	Leu	Lys	Asp	Pro	Glu 565	Lys	Thr	Gln	Glu	Ala 570
Leu	Asp	Ser	Asp	Gly 575	Trp	Leu	His	Thr	Gly 580	Asp	Ile	Gly	Arg	Trp 585
Leu	Pro	Asn	Gly	Thr 590	Leu	Lys	Ile	Ile	Asp 595	Arg	Lys	Lys	Asn	Ile 600
Phe	Lys	Leu	Ala	Gln 605	Gly	Glu	Tyr	Ile	Ala 610	Pro	Glu	Lys	Ile	Glu 615

Asn	Ile	Tyr	Asn	Arg	Ser	Gln	Pro	Val	Leu	Gln	Ile	Phe	Val	His
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Gly	Glu	Ser	Leu	Arg	Ser	Ser	Leu	Val	Gly	Val	Val	Val	Pro	Asp
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Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
				650					655					660
Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
				665					670					675
Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
				680					685					690
Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
				695					700					705
Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
				710					715					720
Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr	Gln	Ile	Asp	Ser	Leu	Tyr	Glu
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His Ile Gln Asp

<210> 87
 <211> 2725
 <212> DNA
 <213> Homo sapiens

<400> 87
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<210> 88
 <211> 660
 <212> PRT
 <213> Homo sapiens

<400> 88
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 35 40 45
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
 50 55 60
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
 65 70 75
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
 80 85 90
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
 95 100 105
 Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu
 110 115 120
 Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val
 125 130 135

Leu Asn Gln Ala Thr Gly His Val Met	Ala Lys Arg Val Phe Asp
140	145 150
Thr Tyr Ser Pro His Glu Asp Glu Ala Met	Val Leu Phe Leu Asn
155	160 165
Met Val Ala Pro Gly Arg Val Leu Ile Cys	Thr Val Lys Asp Glu
170	175 180
Gly Ser Phe His Leu Lys Asp Thr Ala Lys	Ala Leu Leu Arg Ser
185	190 195
Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly	Trp Arg Asp Thr Trp
200	205 210
Ala Phe Val Gly Arg Lys Gly Gly Pro Val	Phe Gly Glu Lys His
215	220 225
Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly	Asp Pro Val Leu Leu
230	235 240
Lys Thr Asp Val Pro Leu Ser Ser Ala Glu	Glu Ala Glu Cys His
245	250 255
Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg	Arg Arg Phe Cys Ser
260	265 270
Lys Val Glu Gly Tyr Gly Ser Val Cys Ser	Cys Lys Asp Pro Thr
275	280 285
Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro	Asp Asn Lys Val Leu
290	295 300
Asn Val Pro Val Ala Val Ile Ala Gly Asn	Arg Pro Asn Tyr Leu
305	310 315
Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala	Gln Gly Val Ser Pro
320	325 330
Gln Met Ile Thr Val Phe Ile Asp Gly Tyr	Tyr Glu Glu Pro Met
335	340 345
Asp Val Val Ala Leu Phe Gly Leu Arg Gly	Ile Gln His Thr Pro
350	355 360
Ile Ser Ile Lys Asn Ala Arg Val Ser Gln	His Tyr Lys Ala Ser
365	370 375
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu	Ala Lys Phe Ala Val
380	385 390
Val Leu Glu Glu Asp Leu Asp Ile Ala Val	Asp Phe Phe Ser Phe
395	400 405
Leu Ser Gln Ser Ile His Leu Leu Glu Glu	Asp Asp Ser Leu Tyr
410	415 420
Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr	Glu His Thr Ala Glu

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			440						445					450
Trp	Val	Leu	Arg	Arg	Ser	Leu	Tyr	Lys	Glu	Glu	Leu	Glu	Pro	Lys
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Trp	Pro	Thr	Pro	Glu	Lys	Leu	Trp	Asp	Trp	Asp	Met	Trp	Met	Arg
			470						475					480
Met	Pro	Glu	Gln	Arg	Arg	Gly	Arg	Glu	Cys	Ile	Ile	Pro	Asp	Val
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Ser	Arg	Ser	Tyr	His	Phe	Gly	Ile	Val	Gly	Leu	Asn	Met	Asn	Gly
			500						505					510
Tyr	Phe	His	Glu	Ala	Tyr	Phe	Lys	Lys	His	Lys	Phe	Asn	Thr	Val
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Pro	Gly	Val	Gln	Leu	Arg	Asn	Val	Asp	Ser	Leu	Lys	Lys	Glu	Ala
			530						535					540
Tyr	Glu	Val	Glu	Val	His	Arg	Leu	Leu	Ser	Glu	Ala	Glu	Val	Leu
			545						550					555
Asp	His	Ser	Lys	Asn	Pro	Cys	Glu	Asp	Ser	Phe	Leu	Pro	Asp	Thr
			560						565					570
Glu	Gly	His	Thr	Tyr	Val	Ala	Phe	Ile	Arg	Met	Glu	Lys	Asp	Asp
			575						580					585
Asp	Phe	Thr	Thr	Trp	Thr	Gln	Leu	Ala	Lys	Cys	Leu	His	Ile	Trp
			590						595					600
Asp	Leu	Asp	Val	Arg	Gly	Asn	His	Arg	Gly	Leu	Trp	Arg	Leu	Phe
			605						610					615
Arg	Lys	Lys	Asn	His	Phe	Leu	Val	Val	Gly	Val	Pro	Ala	Ser	Pro
			620						625					630
Tyr	Ser	Val	Lys	Lys	Pro	Pro	Ser	Val	Thr	Pro	Ile	Phe	Leu	Glu
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Pro	Pro	Pro	Lys	Glu	Glu	Gly	Ala	Pro	Gly	Ala	Pro	Glu	Gln	Thr
			650						655					660

<210> 89
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 89

<400> 94

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<210> 95
 <211> 307
 <212> PRT
 <213> Homo sapiens

<400> 95
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 35 40 45
 Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
 50 55 60
 Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
 65 70 75
 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
 80 85 90
 Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His
 95 100 105
 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
 110 115 120
 Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
 125 130 135
 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
 140 145 150
 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
 155 160 165
 Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
 170 175 180
 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
 185 190 195
 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
 200 205 210
 Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
 215 220 225
 Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

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Asn Ala Thr Gly	Val Ala Met Leu Phe	Ser Ala Gly Thr Phe	Leu
	245	250	255
Tyr Val Ala Thr	Val His Val Leu Pro	Glu Val Gly Gly Ile	Gly
	260	265	270
His Ser His Lys	Pro Asp Ala Thr Gly	Gly Arg Gly Leu Ser	Arg
	275	280	285
Leu Glu Val Ala	Ala Leu Val Leu Gly	Cys Leu Ile Pro Leu	Ile
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Leu Ser Val Gly	His Gln His		
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<210> 96
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 96
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<210> 97
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 97
 ctgtgctcat gttcatggac aactg 25

<210> 98
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 98
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<210> 99
 <211> 1429

<212> DNA

<213> Homo sapiens

<400> 99

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<210> 100
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35 40 45
Ile Met Glu Leu Glu Gly Arg Val Arg Arg Ala Ala Ala Glu Arg
50 55 60
Gly Ala Val Glu Leu Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu
65 70 75
Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser Ser His Asn Phe
80 85 90
Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu Lys Ala Val
95 100 105
Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg Val Leu
110 115 120
Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu Gln
125 130 135
Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg
140 145 150
Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu
155 160 165
Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys
170 175 180
Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp
185 190 195
Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu
200 205 210
Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly
215 220 225
Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser
230 235 240

Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr	
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Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu	
260	265 270
Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val	
275	280 285
Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro	
290	295 300
Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met	
305	310 315
Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu	
320	325 330
Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu	
335	340 345
Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser	
350	355 360
Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile	
365	370 375
Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu	
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Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu	
395	400

<210> 101
 <211> 3671
 <212> DNA
 <213> Homo sapiens

<400> 101
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 ggagctcacc aaccatagca gctgccaaga gccccaggc cctgggtccc 150
 tgccatgggg gagccaaggg aaacctgggg cctgctggat ggcttcccga 200
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 ccagccccag cattcacacg tgccatagaga gcctcctgtc tccctaccct 300
 tcctgggcaa actaagctcc ttgcagagga tcctggagat tcagccccac 350
 catgcccggc tctaccgatc tcaggttgac cctcctacca ccaccatgca 400
 gcgcctcaag gccctcacca ctggctcact gcctaccttt attgatgctg 450
 gtagtaactt cgccagccac gccatagtgg aagacaatct cattaagcag 500

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<210> 102

<211> 1089

<212> PRT

<213> Homo-sapiens

<400> 102

Met	Gln	Lys	Ala	Ser	Val	Leu	Leu	Phe	Leu	Ala	Trp	Val	Cys	Phe	1	5	10	15
Leu	Phe	Tyr	Ala	Gly	Ile	Ala	Leu	Phe	Thr	Ser	Gly	Phe	Leu	Leu	20	25	30	
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro	35	40	45	
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala	50	55	60	
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile	65	70	75	
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val	80	85	90	
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser	95	100	105	
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu	110	115	120	
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu	125	130	135	
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly	140	145	150	
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys	155	160	165	
Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp	170	175	180	
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe	185	190	195	
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly				

				200						205					210
Ile	Leu	Glu	His	Leu 215	Tyr	Pro	Thr	Met	Asp 220	Ser	Gly	Glu	Trp	Asp 225	
Val	Leu	Ile	Ala	His 230	Phe	Leu	Gly	Val	Asp 235	His	Cys	Gly	His	Lys 240	
His	Gly	Pro	His	His 245	Pro	Glu	Met	Ala	Lys 250	Lys	Leu	Ser	Gln	Met 255	
Asp	Gln	Val	Ile	Gln 260	Gly	Leu	Val	Glu	Arg 265	Leu	Glu	Asn	Asp	Thr 270	
Leu	Leu	Val	Val	Ala 275	Gly	Asp	His	Gly	Met 280	Thr	Thr	Asn	Gly	Asp 285	
His	Gly	Gly	Asp	Ser 290	Glu	Leu	Glu	Val	Ser 295	Ala	Ala	Leu	Phe	Leu 300	
Tyr	Ser	Pro	Thr	Ala 305	Val	Phe	Pro	Ser	Thr 310	Pro	Pro	Glu	Glu	Pro 315	
Glu	Val	Ile	Pro	Gln 320	Val	Ser	Leu	Val	Pro 325	Thr	Leu	Ala	Leu	Leu 330	
Leu	Gly	Leu	Pro	Ile 335	Pro	Phe	Gly	Asn	Ile 340	Gly	Glu	Val	Met	Ala 345	
Glu	Leu	Phe	Ser	Gly 350	Gly	Glu	Asp	Ser	Gln 355	Pro	His	Ser	Ser	Ala 360	
Leu	Ala	Gln	Ala	Ser 365	Ala	Leu	His	Leu	Asn 370	Ala	Gln	Gln	Val	Ser 375	
Arg	Phe	Leu	His	Thr 380	Tyr	Ser	Ala	Ala	Thr 385	Gln	Asp	Leu	Gln	Ala 390	
Lys	Glu	Leu	His	Gln 395	Leu	Gln	Asn	Leu	Phe 400	Ser	Lys	Ala	Ser	Ala 405	
Asp	Tyr	Gln	Trp	Leu 410	Leu	Gln	Ser	Pro	Lys 415	Gly	Ala	Glu	Ala	Thr 420	
Leu	Pro	Thr	Val	Ile 425	Ala	Glu	Leu	Gln	Gln 430	Phe	Leu	Arg	Gly	Ala 435	
Arg	Ala	Met	Cys	Ile 440	Glu	Ser	Trp	Ala	Arg 445	Phe	Ser	Leu	Val	Arg 450	
Met	Ala	Gly	Gly	Thr 455	Ala	Leu	Leu	Ala	Ala 460	Ser	Cys	Phe	Ile	Cys 465	
Leu	Leu	Ala	Ser	Gln 470	Trp	Ala	Ile	Ser	Pro 475	Gly	Phe	Pro	Phe	Cys 480	
Pro	Leu	Leu	Leu	Thr 485	Pro	Val	Ala	Trp	Gly 490	Leu	Val	Gly	Ala	Ile 495	

Ala Tyr Ala Gly Leu Leu Gly Thr Ile Glu Leu Lys Leu Asp Leu
500 505 510

Val Leu Leu Gly Ala Val Ala Ala Val Ser Ser Phe Leu Pro Phe
515 520 525

Leu Trp Lys Ala Trp Ala Gly Trp Gly Ser Lys Arg Pro Leu Ala
530 535 540

Thr Leu Phe Pro Ile Pro Gly Pro Val Leu Leu Leu Leu Leu Phe
545 550 555

Arg Leu Ala Val Phe Phe Ser Asp Ser Phe Val Val Ala Glu Ala
560 565 570

Arg Ala Thr Pro Phe Leu Leu Gly Ser Phe Ile Leu Leu Leu Val
575 580 585

Val Gln Leu His Trp Glu Gly Gln Leu Leu Pro Pro Lys Leu Leu
590 595 600

Thr Met Pro Arg Leu Gly Thr Ser Ala Thr Thr Asn Pro Pro Arg
605 610 615

His Asn Gly Ala Tyr Ala Leu Arg Leu Gly Ile Gly Leu Leu Leu
620 625 630

Cys Thr Arg Leu Ala Gly Leu Phe His Arg Cys Pro Glu Glu Thr
635 640 645

Pro Val Cys His Ser Ser Pro Trp Leu Ser Pro Leu Ala Ser Met
650 655 660

Val Gly Gly Arg Ala Lys Asn Leu Trp Tyr Gly Ala Cys Val Ala
665 670 675

Ala Leu Val Ala Leu Leu Ala Ala Val Arg Leu Trp Leu Arg Arg
680 685 690

Tyr Gly Asn Leu Lys Ser Pro Glu Pro Pro Met Leu Phe Val Arg
695 700 705

Trp Gly Leu Pro Leu Met Ala Leu Gly Thr Ala Ala Tyr Trp Ala
710 715 720

Leu Ala Ser Gly Ala Asp Glu Ala Pro Pro Arg Leu Arg Val Leu
725 730 735

Val Ser Gly Ala Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu
740 745 750

Ala Ala Ser Gly Leu Ala Leu Leu Leu Trp Lys Pro Val Thr Val
755 760 765

Leu Val Lys Ala Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu
770 775 780

Thr Pro Phe Ser Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr

785					790					795				
Val	Val	Pro	Gln	Ile	Tyr	Arg	His	Met	Gln	Glu	Glu	Phe	Arg	Gly
				800					805					810
Arg	Leu	Glu	Arg	Thr	Lys	Ser	Gln	Gly	Pro	Leu	Thr	Val	Ala	Ala
				815					820					825
Tyr	Gln	Leu	Gly	Ser	Val	Tyr	Ser	Ala	Ala	Met	Val	Thr	Ala	Leu
				830					835					840
Thr	Leu	Leu	Ala	Phe	Pro	Leu	Leu	Leu	Leu	His	Ala	Glu	Arg	Ile
				845					850					855
Ser	Leu	Val	Phe	Leu	Leu	Leu	Phe	Leu	Gln	Ser	Phe	Leu	Leu	Leu
				860					865					870
His	Leu	Leu	Ala	Ala	Gly	Ile	Pro	Val	Thr	Thr	Pro	Gly	Pro	Phe
				875					880					885
Thr	Val	Pro	Trp	Gln	Ala	Val	Ser	Ala	Trp	Ala	Leu	Met	Ala	Thr
				890					895					900
Gln	Thr	Phe	Tyr	Ser	Thr	Gly	His	Gln	Pro	Val	Phe	Pro	Ala	Ile
				905					910					915
His	Trp	His	Ala	Ala	Phe	Val	Gly	Phe	Pro	Glu	Gly	His	Gly	Ser
				920					925					930
Cys	Thr	Trp	Leu	Pro	Ala	Leu	Leu	Val	Gly	Ala	Asn	Thr	Phe	Ala
				935					940					945
Ser	His	Leu	Leu	Phe	Ala	Val	Gly	Cys	Pro	Leu	Leu	Leu	Leu	Trp
				950					955					960
Pro	Phe	Leu	Cys	Glu	Ser	Gln	Gly	Leu	Arg	Lys	Arg	Gln	Gln	Pro
				965					970					975
Pro	Gly	Asn	Glu	Ala	Asp	Ala	Arg	Val	Arg	Pro	Glu	Glu	Glu	Glu
				980					985					990
Glu	Pro	Leu	Met	Glu	Met	Arg	Leu	Arg	Asp	Ala	Pro	Gln	His	Phe
				995					1000					1005
Tyr	Ala	Ala	Leu	Leu	Gln	Leu	Gly	Leu	Lys	Tyr	Leu	Phe	Ile	Leu
				1010					1015					1020
Gly	Ile	Gln	Ile	Leu	Ala	Cys	Ala	Leu	Ala	Ala	Ser	Ile	Leu	Arg
				1025					1030					1035
Arg	His	Leu	Met	Val	Trp	Lys	Val	Phe	Ala	Pro	Lys	Phe	Ile	Phe
				1040					1045					1050
Glu	Ala	Val	Gly	Phe	Ile	Val	Ser	Ser	Val	Gly	Leu	Leu	Leu	Gly
				1055					1060					1065
Ile	Ala	Leu	Val	Met	Arg	Val	Asp	Gly	Ala	Val	Ser	Ser	Trp	Phe
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Arg Gln Leu Phe Leu Ala Gln Gln Arg
1085

<210> 103
<211> 1743
<212> DNA
<213> Homo sapiens

<400> 103
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ttcaaggagt taaagttact tacactgtgc agtatttcac cacaaattgg 200
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<210> 104
 <211> 442
 <212> PRT
 <213> Homo sapiens

<400> 104
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 35 40 45
 Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser
 50 55 60
 Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu
 65 70 75
 Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His
 80 85 90
 Thr Leu Val Leu Thr Trp Leu Glu Pro Asn Thr Leu Tyr Cys Val
 95 100 105
 His Val Glu Ser Phe Val Pro Gly Pro Pro Arg Arg Ala Gln Pro
 110 115 120
 Ser Glu Lys Gln Cys Ala Arg Thr Leu Lys Asp Gln Ser Ser Glu
 125 130 135
 Phe Lys Ala Lys Ile Ile Phe Trp Tyr Val Leu Pro Ile Ser Ile
 140 145 150
 Thr Val Phe Leu Phe Ser Val Met Gly Tyr Ser Ile Tyr Arg Tyr
 155 160 165

Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile	
				170					175					180	
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	
				185					190					195	
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	
				200					205					210	
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	
				215					220					225	
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	
				230					235					240	
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	
				245					250					255	
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	
				260					265					270	
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	
				275					280					285	
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	
				290					295					300	
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	
				305					310					315	
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	
				320					325					330	
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	
				335					340					345	
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	
				350					355					360	
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	
				365					370					375	
Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser	
				380					385					390	
Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Glu	Gly	
				395					400					405	
Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro	
				410					415					420	
Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly	
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Leu	Tyr	Val	Gln	Met	Glu	Asn									
				440											

<210> 105

<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct

<400> 105
cgctgctgct gttgctcctg g 21

<210> 106
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 106
cagtgtgccca ggactttg 18

<210> 107
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 107
agtcgcaggc agcgttgg 18

<210> 108
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 108
ctcctccgag tctgtgtgct cctgc 25

<210> 109
<211> 51
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

<222> 1-51

<223> Synthetic construct.

<400> 109

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c 51

<210> 110

<211> 1114

<212> DNA

<213> Homo sapiens

<400> 110

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cgcagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100

tctgctgact gtggccaccg ccctgatgct gcccgtagaag cccccgcag 150

gctcctgggg ggcccagatc atcgggggccc acgaggtgac cccccactcc 200

aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250

cttctgctg cgagcccgtt ggggtggtctc ggccgcccac tgcttcagcc 300

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cacctgacac ttaccatgct ctgcacccgc agtggggaca gccacagacg 700

gggcttctgc tcggccgact ccggaggggc cctggtgtgc aggaaccggg 750

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cccgacgtgt acacgcagg gtccgccttt gtggcctgga tctgggacgt 850

ggttcggcgg agcagtcctc agcccgccc cctgcctggg accaccaggc 900

ccccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950

gccgtccag gcctggaatg ttccgtgggt gggccccacg ggaagcctga 1000

tggtcagggt tggggtggga cgggcagcgg tggggcacac ccattccaca 1050

tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
275 280

<210> 112
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 112
gacgtctgca acagctcctg gaag 24

<210> 113
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 113
cgagaaggaa acgaggccgt gag 23

<210> 114
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 114
tgacacttac catgctctgc acccgagtg gggacagcca caga 44

<210> 115
<211> 1808
<212> DNA
<213> Homo sapiens

<400> 115
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cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150
tatgtcaccg gtggggcttg cccagcaag gccaccatcc ctgggaagac 200

ggtcatcgtg acgggcgcca acacagggcat cgggaagcag accgccttgg 250
 aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300
 aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350
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 aacgcgggtg tgatgcgggtg cccccactgg accaccgagg acggcttcga 500
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gctcattt 1808

<210> 116
<211> 331
<212> PRT
<213> Homo sapiens

<400> 116
Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala
1 5 10 15
Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys
20 25 30
Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
35 40 45
Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
50 55 60
Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
65 70 75
Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
80 85 90
Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
95 100 105
Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
110 115 120
Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
125 130 135
Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
140 145 150
Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
155 160 165
Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
170 175 180
His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
185 190 195
Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
200 205 210
Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
215 220 225

agatgccttg gatcaattgg cctttgctta tttccgggca ggaaatgttt 750
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[illegible]

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<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
1 5 10 15

Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr
20 25 30

Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
35 40 45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
110 115 120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
185 190 195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
200 205 210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
215 220 225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
230 235 240

Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu	245	250	255
Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr	260	265	270
Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala	275	280	285
Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr	290	295	300
Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr	305	310	315
Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala	320	325	330
Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu	335	340	345
Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala	350	355	360
Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val	365	370	375
Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser	380	385	390
Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr	395	400	405
Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro	410	415	420
Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly	425	430	435
His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro	440	445	450
Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile	455	460	465
Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr	470	475	480
Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp	485	490	495
Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His	500	505	510
Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys	515	520	525
Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser			

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 tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcat 1700
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<210> 123
 <211> 294
 <212> PRT
 <213> Homo sapiens

<400> 123
 Met Pro Arg Gly Asp Ser Glu Gln Val Arg Tyr Cys Ala Arg Phe
 1 5 10 15
 Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val
 20 25 30
 Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala
 35 40 45
 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu
 50 55 60
 Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met
 65 70 75
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr
 80 85 90
 Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met
 95 100 105
 Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr
 110 115 120
 Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr
 125 130 135
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys
 140 145 150
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys
 155 160 165
 Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly
 170 175 180
 Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn
 185 190 195
 Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val
 200 205 210
 Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile
 215 220 225
 Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

	230		235		240									
Ile	Leu	Leu	Pro	Gln	Phe	Leu	Gly	Val	Leu	Leu	Thr	Leu	Leu	Tyr
				245					250					255
Ile	Thr	Arg	Val	Glu	Asp	Ile	Ile	Met	Glu	His	Ser	Val	Thr	Asp
				260					265					270
Gly	Leu	Leu	Gly	Pro	Gly	Ala	Lys	Pro	Ser	Val	Glu	Ala	Ala	Gly
				275					280					285
Thr	Gly	Cys	Cys	Leu	Cys	Tyr	Pro	Asn						
				290										

<210> 124
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 124
 atcatctatt ccaccgtgtt ctggc 25

<210> 125
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 125
 gacagagtgc tccatgatga tgtcc 25

<210> 126
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 126
 cctgtctgtg ggcattctatg cagagggtga gcggcagaaa tataaaaccc 50

<210> 127
 <211> 1636
 <212> DNA
 <213> Homo sapiens

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<400> 127
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ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtcccac 150
tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300
ggtgaacacc gtccctgaagc acatcatctg gctgaaggct atcacagcta 350
acatcctcca gctgcagggtg aagccctcgg ccaatgacca ggagctgcta 400
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctgggtcaa 450
gaccatcgtg gaggttccaca tgacgactga ggccaagcc accatccgca 500
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ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccttcaat 700
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<210> 128
<211> 484
<212> PRT
<213> Homo sapiens

<400> 128
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Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile
20 25 30
Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys
35 40 45
Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser
50 55 60
Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser
65 70 75
Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile
80 85 90
Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp
95 100 105
Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe
110 115 120
Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr
125 130 135
Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro
140 145 150
Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu
155 160 165
Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu
170 175 180
Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu
185 190 195
Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly
200 205 210
Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu
215 220 225

Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys
230 235 240

Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser
245 250 255

Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu
260 265 270

Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser
275 280 285

Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu
290 295 300

Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His
305 310 315

Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp
320 325 330

Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr
335 340 345

Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu
350 355 360

Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu
365 370 375

Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr
380 385 390

Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp
395 400 405

Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp
410 415 420

Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu
425 430 435

Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu
440 445 450

Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys
455 460 465

Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser
470 475 480

Pro Val Ser Gln

<210> 129
<211> 2213
<212> DNA
<213> Homo sapiens

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 gaacaccatt cttcagagca cacgtctagc cctcagcaag acagttgttt 1600
 ctctctctcc ttgcatattt cctactgcgc tccagcctga gtgatagagt 1650
 gagactctgt ctcaaaaaaa agtatctcta aatacaggat tataatttct 1700
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 aaattagagt ttgtcactta ttccatttgt acctaagaga aaaataggct 1900
 cagttagaaa aggactccct ggccaggcgc agtgacttac gcctgtaatc 1950
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 gaccatcctg gccaacatgg tgaaaccccg tctctactaa aaatataaaa 2050
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 agatcacgcc actgcactcc agcctggcaa cagagcgaga ctccatctca 2200
 aaaaaaaaaa aaa 2213

<210> 130
 <211> 335
 <212> PRT
 <213> Homo sapiens

<400> 130
 Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val
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 Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln
 20 25 30
 Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met
 35 40 45
 Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
 50 55 60
 Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile
 65 70 75
 Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys
 80 85 90
 Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg
 95 100 105

Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp
110 115 120

Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser
125 130 135

Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg
140 145 150

Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln
155 160 165

Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val
170 175 180

Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu
185 190 195

Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met
200 205 210

Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys
215 220 225

Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg
230 235 240

Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn
245 250 255

Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His
260 265 270

Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu
275 280 285

Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys
290 295 300

Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser
305 310 315

Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr
320 325 330

Ser Phe Leu Met Ser
335

<210> 131
<211> 2476
<212> DNA
<213> Homo sapiens

<400> 131
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cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200
cagccaaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250
aggttaacat ttcattccagg aagtcaggta gtgaaacttc cttttatcaa 300
ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350
caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400
ttaacagaat cttggaataa ttttaagggt ctagatccaa attatacaac 450
atggatggat gtcattggaga ggcatggcta ccgaacacag aaatttggga 500
aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550
tggacaagag atgttgcttt cttactcaga caagaaggca ggcccatggt 600
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tttattatgc tatgtgtgct gagacagatg ccatgcttgg tgaaattatt 1000
ttggcccttc atcaattaga tcttcttcag aaaactattg tcatatactc 1050
ctcagaccat ggagagctgg ccatggaaca tcgacagttt tataaaatga 1100
gcatgtacga ggctagtga catgttccgc ttttgatgat gggaccagga 1150
attaaagccg gcctacaagt atcaaagtgt gtttctcttg tggatattta 1200
ccctaccatg cttgatattg ctggaattcc tctgcctcag aacctgagtg 1250
gatactcttt gttgccgtta tcatcagaaa catttaagaa tgaacataaa 1300
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cctattcggg tgggtgcatc atattgcctc aactctttga tctttcctcg 1450
gatccagatg aattaacaaa tgttgctgta aaatttccag aaattactta 1500
ttctttggat cagaagcttc attccattat aaactaccct aaagtttctg 1550

cttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaagt 1600
 ataggacaga attattcaaa cgttatagca aatcttaggt ggcaccaaga 1650
 ctggcagaag gaaccaagga agtatgaaaa tgcaattgat cagtggctta 1700
 aaacccatat gaatccaaga gcagtttgaa caaaaagttt aaaaatagtg 1750
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 atgaaacagt ttttaataatt accaagtttt ggccggggcac agtggctcac 1850
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 tattttgtaa gaatgtagtg tattttaaga taaaatgcc aatgattataa 2200
 aatcacatat tttcaaaaat gggtattatt taggcctttg tacaatttct 2250
 aacaatttag tggaagtatc aaaaggattg aagcaaatac tgtaacagtt 2300
 atgttccttt aaataataga gaatataaaa tattgtaata atatgtatca 2350
 taaaatagtt gtatgtgagc atttgatggt gaaaaaaaaa aaaaaaaaaa 2400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2450
 aaaaaaaaaa aaaaaaaaaa aaaaaa 2476

<210> 132
 <211> 536
 <212> PRT
 <213> Homo sapiens

<400> 132
 Met Leu Leu Leu Trp Val Ser Val Val Ala Ala Leu Ala Leu Ala
 1 5 10 15
 Val Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys
 20 25 30
 Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg
 35 40 45
 Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile
 50 55 60
 Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr
 65 70 75

Asn Ser Pro Ile Cys Cys Pro Ser Arg Ala Ala Met Trp Ser Gly	80	85	90
Leu Phe Thr His Leu Thr Glu Ser Trp Asn Asn Phe Lys Gly Leu	95	100	105
Asp Pro Asn Tyr Thr Thr Trp Met Asp Val Met Glu Arg His Gly	110	115	120
Tyr Arg Thr Gln Lys Phe Gly Lys Leu Asp Tyr Thr Ser Gly His	125	130	135
His Ser Ile Ser Asn Arg Val Glu Ala Trp Thr Arg Asp Val Ala	140	145	150
Phe Leu Leu Arg Gln Glu Gly Arg Pro Met Val Asn Leu Ile Arg	155	160	165
Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp Trp Gln Asn Thr	170	175	180
Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile Asn Tyr Thr	185	190	195
Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His Pro Tyr	200	205	210
Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe His	215	220	225
Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys	230	235	240
Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr	245	250	255
Tyr Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys	260	265	270
Glu Ile Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu	275	280	285
Thr Asp Ala Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu	290	295	300
Asp Leu Leu Gln Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly	305	310	315
Glu Leu Ala Met Glu His Arg Gln Phe Tyr Lys Met Ser Met Tyr	320	325	330
Glu Ala Ser Ala His Val Pro Leu Leu Met Met Gly Pro Gly Ile	335	340	345
Lys Ala Gly Leu Gln Val Ser Asn Val Val Ser Leu Val Asp Ile	350	355	360
Tyr Pro Thr Met Leu Asp Ile Ala Gly Ile Pro Leu Pro Gln Asn			

atccccgagcc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500
 ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggatac 550
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 tggagaggct ctttacttgg gcattatttc ttccctgttc tccctgatag 650
 ctggaatcat cctctgcttt tctgtctcat cccagagaaa tcgctccaac 700
 tactacgatg cctaccaagc ccaacctctt gccacaagga gctctccaag 750
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 cagggtatgt gtgaagaacc aggggccaga gctgggggggt ggctgggtct 850
 gtgaaaaaca gtggacagca ccccgagggc cacagggtgag ggacactacc 900
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 ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga 1000
 attgccaaag atgctcgcca tgccagcctt tctgttttcc tcaccttgct 1050
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 agccaggact cagaggatcc ctttgccctc tggtttacct gggactccat 1150
 ccccaaacc actaatcaca tccactgac tgaccctctg tgatcaaaga 1200
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 actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc 1400
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 gcagcctggg acatttaaaa aaata 1475

<210> 134
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 134
 Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu
 1 5 10 15
 Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp
 20 25 30
 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly
 35 40 45
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

50	55	60
Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala		
65	70	75
Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile		
80	85	90
Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met Arg Cys Thr		
95	100	105
Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala Val Ala		
110	115	120
Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro		
125	130	135
Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro		
140	145	150
Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr		
155	160	165
Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile		
170	175	180
Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr		
185	190	195
Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg		
200	205	210
Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser		
215	220	225
Leu Thr Gly Tyr Val		
230		

<210> 135
 <211> 610
 <212> DNA
 <213> Homo sapiens

<400> 135
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 aagtcacgcg tcccgctggc tcagaacccat ggctgtgcca gccggcacc 150
 aggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200
 cgccatcgtg tccctgagcg agaccgcga atgtggtccc ccctgcacct 250
 tctggccctg ctttgagctc tgctgtcttg attcctttgg cctcaciaaac 300
 gattttgttg tgaagctgaa gggtcagggt gtgaattccc agtgccactc 350

atctcccatc tccagtaa at gtgaaagcag aagacgtttt ccctgagaag 400
 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
 atgacagtag attatcagga aataaataaa gtgggtttttc caatgtacac 600
 acctgtaaaa 610

<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
 1 5 10 15
 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
 65 70 75
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
 80 85 90
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
 95 100 105
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
 110 115

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
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 gtctttgccca ttttctgcat ctccaggctc ctctgtctcac acggagcccc 100
 agtggccccc atgactcctt acctgatgct gtgccagcca cacaagagat 150
 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200
 gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

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 ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600
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 accccaaggc tggctgggga acccttcacc cttctgtgag attttccatc 700
 atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750
 tatgtacttt ataatgaaa a 771

<210> 138
 <211> 110
 <212> PRT
 <213> Homo sapiens.

<400> 138
 Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys
 1 5 10 15
 Ile Ser Arg Leu Leu Cys Ser His Gly Ala Pro Val Ala Pro Met
 20 25 30
 Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp
 35 40 45
 Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val
 50 55 60
 Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg
 65 70 75
 Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu
 80 85 90
 Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu
 95 100 105
 Cys Arg Ser Val Ser
 110

<210> 139
 <211> 2044
 <212> DNA
 <213> Homo sapiens

<400> 139

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 ctccccggca ccagaagtcc ctctgcgcgt ccgacggcga catgggcgctc 150
 cccacggccc tggaggccgg cagctggcgc tggggatccc tgcctcttcgc 200
 tctcttctctg gctgcgtccc taggtccggg ggcagccttc aaggctcgcca 250
 cgcggtatcc cctgtatgtc tgtcccagg ggcagaacgt caccctcacc 300
 tgcaggctct tgggccctgt ggacaaaggg cagcatgtga ccttctacaa 350
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 caccaggctg ccaacaccag ccacgacctg gctcagcgcc acgggctgga 500
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 agattctccc ctagagacct gaaattcacc agctacagat gccaaatgac 1350
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 tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450

140										145					150				
Ile	Arg	His	His	His	Ser	Glu	His	Arg	Val	His	Gly	Ala	Met	Glu					
				155					160					165					
Leu	Gln	Val	Gln	Thr	Gly	Lys	Asp	Ala	Pro	Ser	Asn	Cys	Val	Val					
				170					175					180					
Tyr	Pro	Ser	Ser	Ser	Gln	Asp	Ser	Glu	Asn	Ile	Thr	Ala	Ala	Ala					
				185					190					195					
Leu	Ala	Thr	Gly	Ala	Cys	Ile	Val	Gly	Ile	Leu	Cys	Leu	Pro	Leu					
				200					205					210					
Ile	Leu	Leu	Leu	Val	Tyr	Lys	Gln	Arg	Gln	Ala	Ala	Ser	Asn	Arg					
				215					220					225					
Arg	Ala	Gln	Glu	Leu	Val	Arg	Met	Asp	Ser	Asn	Ile	Gln	Gly	Ile					
				230					235					240					
Glu	Asn	Pro	Gly	Phe	Glu	Ala	Ser	Pro	Pro	Ala	Gln	Gly	Ile	Pro					
				245					250					255					
Glu	Ala	Lys	Val	Arg	His	Pro	Leu	Ser	Tyr	Val	Ala	Gln	Arg	Gln					
				260					265					270					
Pro	Ser	Glu	Ser	Gly	Arg	His	Leu	Leu	Ser	Glu	Pro	Ser	Thr	Pro					
				275					280					285					
Leu	Ser	Pro	Pro	Gly	Pro	Gly	Asp	Val	Phe	Phe	Pro	Ser	Leu	Asp					
				290					295					300					
Pro	Val	Pro	Asp	Ser	Pro	Asn	Phe	Glu	Val	Ile									
				305					310										

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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 cttagacctc ctttctgcc ctcttttctt gccaccgct gcttcttggc 150
 ccttctccga ccccgctcta gcagcagacc tcctggggtc tgtgggttga 200
 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgact 250
 ccgctcccg accagcgcc tgaccctggg gaaaggatgg ttcccgaggt 300
 gagggctctc tcctccttgc tgggactcgc gctgctctgg ttccccctgg 350
 actccacgc tcgagccgc ccagacatgt tctgcctttt ccatgggaag 400
 agatactccc ccggcgagag ctggcacccc tacttggagc cacaaggcct 450

gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttggt 500
accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550
cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600
ggccccacca aagtcctgcc agcacaacgg gaccatgtac caacacggag 650
agatcttcag tgcccatgag ctgttccct cccgcctgcc caaccagtgt 700
gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750
ccccgaacca ggctgcccag caccctccc actgccagac tctgtctgcc 800
aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850
cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgatgc 900
tgggagaaaag agaggcccg gcacccagc cccactggc ctcagcgccc 950
ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca 1000
actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050
cgggaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct 1100
tcggccccct gccctgcac ctatgcacct gtgaggatgg ccgccaggac 1150
tgccagcgtg tgacctgtcc caccgagtac ccctgccgtc accccgagaa 1200
agtggctggg aagtgtgca agatttgccc agaggacaaa gcagaccctg 1250
gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300
ctcgtccaca catcgggtat cccaagccca gacaacctgc gtcgctttgc 1350
cctggaacac gaggcctcgg acttggtgga gatctacctc tggaagctgg 1400
taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450
ccacacagcc agaattcttc acttgactca gatcaagaaa gtcaggaagc 1500
aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac 1550
gaaggctcact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600
ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650
gatatgagct gtataattgt tgttattata tattaataaa taagaagttg 1700
cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142
<211> 451
<212> PRT
<213> Homo sapiens
<400> 142

[illegible]

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Arg	His	Pro	Glu	Lys 305	Val	Ala	Gly	Lys	Cys 310	Cys	Lys	Ile	Cys	Pro 315	
Glu	Asp	Lys	Ala	Asp 320	Pro	Gly	His	Ser	Glu 325	Ile	Ser	Ser	Thr	Arg 330	
Cys	Pro	Lys	Ala	Pro 335	Gly	Arg	Val	Leu	Val 340	His	Thr	Ser	Val	Ser 345	
Pro	Ser	Pro	Asp	Asn 350	Leu	Arg	Arg	Phe	Ala 355	Leu	Glu	His	Glu	Ala 360	
Ser	Asp	Leu	Val	Glu 365	Ile	Tyr	Leu	Trp	Lys 370	Leu	Val	Lys	Asp	Glu 375	
Glu	Thr	Glu	Ala	Gln 380	Arg	Gly	Glu	Val	Pro 385	Gly	Pro	Arg	Pro	His 390	
Ser	Gln	Asn	Leu	Pro 395	Leu	Asp	Ser	Asp	Gln 400	Glu	Ser	Gln	Glu	Ala 405	
Arg	Leu	Pro	Glu	Arg 410	Gly	Thr	Ala	Leu	Pro 415	Thr	Ala	Arg	Trp	Pro 420	
Pro	Arg	Arg	Ser	Leu 425	Glu	Arg	Leu	Pro	Ser 430	Pro	Asp	Pro	Gly	Ala 435	
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Thr

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<210> 143
<211> 693
<212> DNA
<213> Homo sapiens
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tgggctacgc gctcctcggt atcgtgaccc cgggagagcg gcggaagcag 200
gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250
ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300
cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350
ggcgccagcg ggaggtcacc gtgagaccgg acttgctctc gtgggcgccg 400
gaccttggtt tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450
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gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550
 ttttaaggtcc gcaaggcggg ccaggggccga gacgcgagtc ggatgtggtg 600
 aactgaaaga accaataaaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 144
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 20 25 30
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
 35 40 45
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
 50 55 60
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
 65 70 75
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
 80 85 90
 Arg Ser Pro

<210> 145
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<400> 145
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 caggctgcca tggggcccag caccctctc ctcatcttgt tccttttgtc 150
 atggtcggga cccctccaag gacagcagca ccaccttggt gagtacatgg 200
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
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 acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

gagaccacaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450
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 gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala
				260					265					270
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala
				275					280					285
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys
				290					295					300
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro
				305					310					315
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr
				320					325					330
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile
				335					340					345
Gln	Cys	Ser	Phe	Asp	Ala	Ser	Gly	Thr	Leu	Thr	Pro	Glu	Arg	Ala
				350					355					360
Ala	Leu	Pro	Tyr	Phe	Pro	Arg	Arg	Tyr	Gly	Ala	His	Ala	Ser	Leu
				365					370					375
Arg	Tyr	Asn	Pro	Arg	Glu	Arg	Gln	Leu	Tyr	Ala	Trp	Asp	Asp	Gly
				380					385					390
Tyr	Gln	Ile	Val	Tyr	Lys	Leu	Glu	Met	Arg	Lys	Lys	Glu	Glu	Glu
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Val

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
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 gttctctctt tctctctaata ccatccgtca cctctcctgt catccgtttc 150
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
 ttgggttctga gtctcctcaa gctgggatca gggcagtggc aggtgttttg 250
 gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct 300
 gtttctctgt tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350
 agggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
 attctattgc ggaggggcgc atctctctga ggctggaaaa cattactgtg 500

ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550
 gaaggccatc tgggagctac aggtgtcagc actggggtca gttcctctca 600
 tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc 650
 tcgggctggt tccccggcc cacagcgaag tggaaaggct cacaaggaca 700
 ggatttgtcc acagactcca ggacaaacag agacatgcat ggcctgtttg 750
 atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt 800
 tccatgcggc atgtctcatct gagccgagag gtggaatcca gggtagagat 850
 aggagatacc tttttcgagc ctatatcgtg gcacctggct accaaagtac 900
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 aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150
 gagatttaca aggaagagtg tgggtggcttc tcagagtttc caagcaggga 1200
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 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950

tgttagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000

acagagtgta tcctaattggt ttgttcatta tattacactt tcagtaaaaa 2050

aa 2052

<210> 148

<211> 500

<212> PRT

<213> Homo sapiens

<400> 148

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Ser	Gly	Gln	Trp	Gln	Val	Phe	Gly	Pro	Asp	Lys	Pro	Val	Gln	Ala
				20					25					30

Leu	Val	Gly	Glu	Asp	Ala	Ala	Phe	Ser	Cys	Phe	Leu	Ser	Pro	Lys
				35					40					45

Thr	Asn	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Gly	Gln	Phe
				50					55					60

Ser	Ser	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Lys	Asp	Gln	Pro	Phe
				65					70					75

Met	Gln	Met	Pro	Gln	Tyr	Gln	Gly	Arg	Thr	Lys	Leu	Val	Lys	Asp
				80					85					90

Ser	Ile	Ala	Glu	Gly	Arg	Ile	Ser	Leu	Arg	Leu	Glu	Asn	Ile	Thr
				95					100					105

Val	Leu	Asp	Ala	Gly	Leu	Tyr	Gly	Cys	Arg	Ile	Ser	Ser	Gln	Ser
				110					115					120

Tyr	Tyr	Gln	Lys	Ala	Ile	Trp	Glu	Leu	Gln	Val	Ser	Ala	Leu	Gly
				125					130					135

Ser	Val	Pro	Leu	Ile	Ser	Ile	Thr	Gly	Tyr	Val	Asp	Arg	Asp	Ile
				140					145					150

Gln	Leu	Leu	Cys	Gln	Ser	Ser	Gly	Trp	Phe	Pro	Arg	Pro	Thr	Ala
				155					160					165

Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Thr	Asp	Ser	Arg
				170					175					180

Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu	Ile	Ser	Leu
				185					190					195

Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met	Arg	His
				200					205					210

Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly	Asp
				215					220					225

Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	His	Leu	Ala	Thr	Lys	Val	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

230					235					240				
Gly	Ile	Leu	Cys	Cys	Gly	Leu	Phe	Phe	Gly	Ile	Val	Gly	Leu	Lys
				245					250					255
Ile	Phe	Phe	Ser	Lys	Phe	Gln	Trp	Lys	Ile	Gln	Ala	Glu	Leu	Asp
				260					265					270
Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys
				275					280					285
His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys
				290					295					300
Leu	Cys	Val	Ser	Asp	Leu	Lys	Thr	Val	Thr	His	Arg	Lys	Ala	Pro
				305					310					315
Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val
				320					325					330
Val	Ala	Ser	Gln	Ser	Phe	Gln	Ala	Gly	Lys	His	Tyr	Trp	Glu	Val
				335					340					345
Asp	Gly	Gly	His	Asn	Lys	Arg	Trp	Arg	Val	Gly	Val	Cys	Arg	Asp
				350					355					360
Asp	Val	Asp	Arg	Arg	Lys	Glu	Tyr	Val	Thr	Leu	Ser	Pro	Asp	His
				365					370					375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Asn	Gly	Glu	His	Leu	Tyr	Phe	Thr
				380					385					390
Leu	Asn	Pro	Arg	Phe	Ile	Ser	Val	Phe	Pro	Arg	Thr	Pro	Pro	Thr
				395					400					405
Lys	Ile	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Cys	Gly	Thr	Ile	Ser	Phe
				410					415					420
Phe	Asn	Ile	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Thr	Cys	Arg
				425					430					435
Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Glu	Tyr	Pro	Ser	Tyr	Asn
				440					445					450
Glu	Gln	Asn	Gly	Thr	Pro	Ile	Val	Ile	Cys	Pro	Val	Thr	Gln	Glu
				455					460					465
Ser	Glu	Lys	Glu	Ala	Ser	Trp	Gln	Arg	Ala	Ser	Ala	Ile	Pro	Glu
				470					475					480
Thr	Ser	Asn	Ser	Glu	Ser	Ser	Ser	Gln	Ala	Thr	Thr	Pro	Phe	Leu
				485					490					495
Pro	Arg	Gly	Glu	Met										
				500										

<210> 149
<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gcgtggtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
ggaactgacc cagtgtgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgccca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
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ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150
gcctcgccct gttgtgctgc gccgccgccg ccgccgccgt cgcctcagcc 200
gcctcggcgg ggaatgtcac cggtggcggc ggggccgcgg ggcagggtgga 250
cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttcccta 300
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accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400

cacccctcatt tgggcgactg ctggaccctc ttccaccacc tttcaggcgc 450
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 aaaaggctgc tactctcaag gaccatactg gtttaaacia aggaggatga 1000
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 ctggtttgtt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850

	170		175		180
Ala Thr Glu Ala	Pro Ser Ser Pro Pro	Pro Glu Tyr Val Cys Asn			
	185	190			195
Cys Ser Val Val	Gly Ser Leu Asn Val	Asn Arg Cys Asn Gln Thr			
	200	205			210
Thr Gly Gln Cys	Glu Cys Arg Pro Gly	Tyr Gln Gly Leu His Cys			
	215	220			225
Glu Thr Cys Lys	Glu Gly Phe Tyr Leu	Asn Tyr Thr Ser Gly Leu			
	230	235			240
Cys Gln Pro Cys	Asp Cys Ser Pro His	Gly Ala Leu Ser Ile Pro			
	245	250			255

Cys Asn Arg

<210> 154
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 154
 aactgctctg tggttggaag cctg 24

<210> 155
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 155
 cagtcacatg gctgacagac ccac 24

<210> 156
 <211> 38
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-38
 <223> Synthetic construct.

<400> 156
 aggttatcag gggcttcact gtgaaacctg caaagagg 38

[illegible]

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<400> 157
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ctggaccctg agcagcttct tgggccctgg tacgtgcttg cgggtggcctc 150
ccgggaaaag ggctttgcc a tggagaagga catgaagaac gtcgtggggg 200
tggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250
cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaag 300
ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350
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cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgcccaca 600
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<400> 158
Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
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Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
 20          25          30

Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35          40          45

Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50          55          60

Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65          70          75

His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80          85          90

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Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu
95 100 105
Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile
110 115 120
Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu
125 130 135
Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu
140 145 150
Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe Leu Ser Gln
155 160

<210> 159
<211> 1665
<212> DNA
<213> Homo sapiens

<400> 159
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gctgctgctg ccctgctctt gggggaggga gagggcggaa ggacagacaa 100
gtaaactgct gacgatgcag agttccgtga cggtgcagga aggcctgtgt 150
gtccatgtgc cctgctcctt ctctacccc tcgcatggct ggatttacc 200
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actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc 400
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550
gtgagcaggg gacacccct atgatctcct ggataggac ctccgtgtcc 600
cccctggacc cctccaccac ccgctcctcg gtgctcacc tcaccccaca 650
gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750
cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850
tggctctgtc agttgatgca gttgacagca atccccctgc caggctgagc 900
ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaacccggg 950

ggtgctggag	ctgccttggg	tgcacctgag	ggatgcagct	gaattcacct	1000
gcagagctca	gaaccctctc	ggctctcagc	aggtctacct	gaacgtctcc	1050
ctgcagagca	aagccacatc	aggagtgact	caggggggtg	tcgggggagc	1100
tggagccaca	gccctggtct	tcctgtcctt	ctgcgtcatc	ttcgtttag	1150
tgaggtcctg	caggaagaaa	tcggcaaggc	cagcagcggg	cgtgggagat	1200
acgggcatag	aggatgcaaa	cgctgtcagg	ggttcagcct	ctcagggggc	1250
cctgactgaa	ccttgggcag	aagacagtcc	cccagaccag	cctccccag	1300
cttctgccc	ctcctcagt	ggggaaggag	agctccagta	tgcatccctc	1350
agcttccaga	tggatgaagc	ttgggactcg	cggggacagg	aggccactga	1400
caccgagtac	tcggagatca	agatccacag	atgagaaact	gcagagactc	1450
accctgattg	agggatcaca	gccctccag	gcaagggaga	agtcagaggc	1500
tgattcttgt	agaattaaca	gccctcaacg	tgatgagcta	tgataacact	1550
atgaattatg	tgacagagtga	aaagcacaca	ggcttttagag	tcaaagtatc	1600
tcaaacctga	atccacactg	tgccctccct	tttatttttt	taactaaaag	1650
acagacaaat	tccta				1665

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<210> 160
<211> 463
<212> PRT
<213> Homo sapiens
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<400>	160													
Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala
1				5					10					15
Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr
				20					25					30
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr
				50					55					60
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala
				65					70					75
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg
				80					85					90
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser
				95					100					105
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg

Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu	110	115	120
125	130	135	
Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile	140	145	150
Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser	155	160	165
Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp	170	175	180
Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser	185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser	200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn	215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr	230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly	245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu	260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu	275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser	290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala	305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln	320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val	335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe	350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys	365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu	380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr	395	400	405

Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala
 410 415 420
 Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser
 425 430 435
 Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu
 440 445 450
 Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg
 455 460

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
 gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50
 accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100
 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150
 tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagtg 200
 aaggtgacag ccctgggcgg tgggaagttg gaagccacgt tcaccttcat 250
 gaggaggat cggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
 gagctgcca ggagggacca ctacatcttt tactgcaaag accagcacca 400
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
 accgggaggc cctggaagaa tttaagaaat tgggtgcagcg caagggactc 500
 tcggaggagg acattttcac gccctgcag acgggaagct gcgttcccg 550
 aactaggca gcccccggt ctgcacctcc agagcccacc ctaccaccag 600
 acacagagcc cggaccacct ggacctaccc tccagccatg acccttcct 650
 gctcccaccc acctgactcc aaataaagtc cttttccccc aaaaaaaaaa 700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
 1 5 10 15
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

<210> 165
<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct.

<400> 165
gtcctccgga aagtccttat c 21

<210> 166
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 166
gcctagtgtt cggaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 167
caggacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 168
ctgtccttca ccctggagga ggaggatatc acaggacct ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169

gttccgcaga tgcagaggtt gaggtggctg cgggactgga agtcacgagg 50
cagaggtctc acagcagcca aggaacctgg ggcccgcctc tccccctcc 100
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150
gtagggggag agaccaggat catcaagggg ttcgagtga agcctcactc 200
ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtgggg 250
cgacgctcat cgccccaga tggctcctga cagcagccca ctgcctcaag 300
ccccgtaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350
ctgtgagcag acccgacag ccaactgagtc cttccccac ccgggttca 400
acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450
atggcatcgc cagtctccat cacctgggct gtgcgacccc tcaccctctc 500
ctcacgctgt gtcactgctg gcaccagctg cctcatttcc ggctggggca 550
gcacgtccag cccccagtta cgctgcctc acaccttgcg atgcgccaac 600
atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650
cacagacacc atgggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
gccaggggtga ctccgggggc cctctgggtc gtaaccagtc tcttcaaggc 750
attatctcct ggggccagga tccgtgtgcg atcaccgaa agcctggtgt 800
ctacacgaaa gtctgcaaat atgtggactg gatccaggag acgatgaaga 850
acaattagac tggaccacc caccacagcc catcacctc catttccact 900
tgggtgtttg ttctgtttca ctctgttaat aagaaaccct aagccaagac 950
cctctacgaa cattcttttg gcctcctgga ctacaggaga tgctgtcact 1000
taataatcaa cctgggggttc gaaatcagtg agacctggat tcaaattctg 1050
ccttgaaata ttgtgactct gggaatgaca acacctggtt tgttctctgt 1100
tgtatcccca gcccacaa gaagctcctgg ccatatatca aggtttcaat 1150
aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
aaaa 1204

<210> 170
<211> 250
<212> PRT
<213> Homo sapiens

<400> 170
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
1 5 10 15

Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro
20 25 30
His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu
35 40 45
Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala
50 55 60
Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His
65 70 75
Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr
80 85 90
Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys
95 100 105
Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro Val
110 115 120
Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys
125 130 135
Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr
140 145 150
Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn
155 160 165
Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly
170 175 180
Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly Gly
185 190 195
Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn
200 205 210
Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala
215 220 225
Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val
230 235 240
Asp Trp Ile Gln Glu Thr Met Lys Asn Asn
245 250

<210> 171
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 171
ggctgcgga ctggaagtca tcggg 25

<210> 172
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 172
ctccaggcca tgaggattct gcag 24

<210> 173
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 173
cctctggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 174
tctgtgatgt tgccggggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 175
cgtgtagaca ccaggctttc ggggtg 25

<210> 176
<211> 18
<212> DNA

<213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 176
 cccttgatga tcctgggc 18

<210> 177
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 177
 aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggcctt 50

<210> 178
 <211> 43
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-43
 <223> Synthetic construct.

<400> 178
 gagagaccag gatcatcaag gggttcagat gcaagcctca ctc 43

<210> 179
 <211> 907
 <212> DNA
 <213> Homo sapiens

<400> 179
 gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50
 gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100
 aagaaagagg agagcaccga agaagtgaag atagaagttt tgcacgtcc 150
 agaaaactgc tctaagacaa gcaagaaggg agacctacta aatgcccatt 200
 atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250
 caaatgaag gccaccccaa atggtttggt cttggtgttg ggcaagtcac 300
 aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350
 aagtagttat acccccttca tttgcatagc gaaaggaagg ctatgcagaa 400

ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450
 tgtgacaaaa ggaccacgga gcattgagac atttaaacia atagacatgg 500
 acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550
 gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600
 tttagaagat atttttaaga agaatgacca tgatgggtgat ggcttcattt 650
 ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700
 atttctactt ttttttttta gctatttact gtactttatg tataaaacia 750
 agtcactttt ctccaagttg tatttgctat ttttccccta tgagaagata 800
 ttttgatctc cccaatacat tgattttggt ataataaatg tgaggctgtt 850
 ttgcaaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
 aaaaaaa 907

<210> 180

<211> 222

<212> PRT

<213> Homo sapiens

<400> 180

Met	Pro	Lys	Thr	Met	His	Phe	Leu	Phe	Arg	Phe	Ile	Val	Phe	Phe	1	5	10	15
Tyr	Leu	Trp	Gly	Leu	Phe	Thr	Ala	Gln	Arg	Gln	Lys	Lys	Glu	Glu	20	25	30	
Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn	35	40	45	
Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr	50	55	60	
Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg	65	70	75	
Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly	80	85	90	
Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro	95	100	105	
Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly	110	115	120	
Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu	125	130	135	
Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser	140	145	150	

Ile Glu Thr Phe Lys Gln Ile Asp Met Asp Asn Asp Arg Gln Leu
155 160 165
Ser Lys Ala Glu Ile Asn Leu Tyr Leu Gln Arg Glu Phe Glu Lys
170 175 180
Asp Glu Lys Pro Arg Asp Lys Ser Tyr Gln Asp Ala Val Leu Glu
185 190 195
Asp Ile Phe Lys Lys Asn Asp His Asp Gly Asp Gly Phe Ile Ser
200 205 210
Pro Lys Glu Tyr Asn Val Tyr Gln His Asp Glu Leu
215 220

<210> 181
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-22
<223> Synthetic construct.

<400> 181
gtgtttctgct ggagccgatg cc 22

<210> 182
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 182
gacatggaca atgacagg 18

<210> 183
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 183
cctttcagga tgtaggag 18

<210> 184
<211> 18
<212> DNA
<213> Artificial

```
<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.
```

```
<400> 184
gatgtctgcc accccaag 18
```

```
<210> 185
<211> 27
<212> DNA
<213> Artificial
```

```
<220>
<221> Artificial Sequence
<222> 1-27
<223> Synthetic construct.
```

```
<400> 185
  gcatcctgat atgacttgtc acgtggc 27
```

```
<210> 186
<211> 24
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.
```

```
<400> 186
tacaagaggg aagaggagtt gcac 24
```

```
<210> 187
<211> 52
<212> DNA
<213> Artificial
```

```
<220>
<221> Artificial Sequence
<222> 1-52
<223> Synthetic construct.
```

```
<400> 187
gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50
cc 52
```

```
<210> 188
<211> 573
<212> DNA
<213> Homo sapiens
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```
<400> 188
cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50
ctctttggag ctgtgactca gaaaaccaa acttctgtg ctaagtgcc 100
```

cccaaatgct tctgtgtca ataacactca ctgcacctgc aaccatggat 150
 atacttctgg atctgggcag aaactattca cattcccctt ggagacatgt 200
 aacgccaggc atggtggctc ggcctgttaa tcccagttct ttgggaagcc 250
 aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300
 atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350
 ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400
 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450
 ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500
 ttcttgtttc atttcgcgac tgccctctca gtgtttcttg ggatcccctc 550
 ccaaataaag tacttatatt ctc 573

<210> 189
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 189
 Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser
 1 5 10 15
 Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
 20 25 30
 Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
 35 40 45
 Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
 50 55 60
 Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
 65 70

<210> 190
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 190
 aggaccatt gcttcttcca ggcc 24

<210> 191
 <211> 24
 <212> DNA
 <213> Artificial


```

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 192
cctgtgctaa gtgccccca aatgcttct gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
caagcaggtc atcccccttg tgaccttcaa agagaagcag agaggggcaga 50
ggtagggggg acagggaaag ggtgacctct gagattcccc ttttccccca 100
gactttggaa gtgaccacc atggggctca gcatcttttt gctcctgtgt 150
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250
gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
gctcactgca gcggcagcag gtactgggtg cgcctggggg aacacagcct 350
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
cccatcccg ctacctggga gcctcgacga gccacgagca cgacctccgg 450
ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccct 500
gcccctgccc aatgactgtg caaccgctgg caccgagtgc cactctcag 550
gctggggcat caccaaccac ccacggaacc cattcccga tctgctccag 600
tgcctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650
cgggagaatc acgagcaaca tgggtgtgtg aggcggcgtc ccggggcagg 700
atgcctgcca gggtgattct gggggcccc tgggtgtgtg gggagtcctt 750
caaggctctg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800

```

ccttgga gtc tacacctata tttgcaagta tgtggactgg atccggatga 850
tcatgaggaa caactgacct gtttccctcca cctccacccc cacccttaa 900
cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950
ccctagctcc actcttggtg gcctgggaac ttcttggaac tttaactcct 1000
gccagccctt ctaagaccca cgagcggggt gagagaagtg tgcaatagtc 1050
tggaataaat ataaatgaag gaggggcaaa aaaaaaaaaa a 1091

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<210> 194
<211> 248
<212> PRT
<213> Homo sapiens
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<400> 194														
Met 1	Gly	Leu	Ser	Ile 5	Phe	Leu	Leu	Leu	Cys 10	Val	Leu	Gly	Leu	Ser 15
Gln	Ala	Ala	Thr	Pro 20	Lys	Ile	Phe	Asn	Gly 25	Thr	Glu	Cys	Gly	Arg 30
Asn	Ser	Gln	Pro	Trp 35	Gln	Val	Gly	Leu	Phe 40	Glu	Gly	Thr	Ser	Leu 45
Arg	Cys	Gly	Gly	Val 50	Leu	Ile	Asp	His	Arg 55	Trp	Val	Leu	Thr	Ala 60
Ala	His	Cys	Ser	Gly 65	Ser	Arg	Tyr	Trp	Val 70	Arg	Leu	Gly	Glu	His 75
Ser	Leu	Ser	Gln	Leu 80	Asp	Trp	Thr	Glu	Gln 85	Ile	Arg	His	Ser	Gly 90
Phe	Ser	Val	Thr	His 95	Pro	Gly	Tyr	Leu	Gly 100	Ala	Ser	Thr	Ser	His 105
Glu	His	Asp	Leu	Arg 110	Leu	Leu	Arg	Leu	Arg 115	Leu	Pro	Val	Arg	Val 120
Thr	Ser	Ser	Val	Gln 125	Pro	Leu	Pro	Leu	Pro 130	Asn	Asp	Cys	Ala	Thr 135
Ala	Gly	Thr	Glu	Cys 140	His	Val	Ser	Gly	Trp 145	Gly	Ile	Thr	Asn	His 150
Pro	Arg	Asn	Pro	Phe 155	Pro	Asp	Leu	Leu	Gln 160	Cys	Leu	Asn	Leu	Ser 165
Ile	Val	Ser	His	Ala 170	Thr	Cys	His	Gly	Val 175	Tyr	Pro	Gly	Arg	Ile 180
Thr	Ser	Asn	Met	Val 185	Cys	Ala	Gly	Gly	Val 190	Pro	Gly	Gln	Asp	Ala 195
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu

200 205 210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp
215 220 225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp
230 235 240
Ile Arg Met Ile Met Arg Asn Asn
245

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<211> 1485
<212> DNA
<213> Homo sapiens

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ggcttgctca aagcccggca ggagaggagg ctggccgaga tcaaccggga 200
gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250
tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350
caagaccac ctggagatga agaagatgat ctgagagggtg acaggagggg 400
tcagtgaac tatatcctac cgagactttg tgaacatgat gctggggaaa 450
cggtcggctg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500
gagcagcccc aagccagttg gccccctcc agagagagac attgctagcc 550
tgccctgagg acccgcctg gactccccag cttcccacc ccatacctcc 600
ctccgatct tgctgccctt cttgacacac tgtgatctct ctctctctca 650
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tgacccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196
<211> 150
<212> PRT
<213> Homo sapiens

<400> 196
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Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu
35 40 45
Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp
50 55 60
Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met
65 70 75
Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys
80 85 90
Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr
95 100 105
Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu
110 115 120
Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro
125 130 135
Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro
140 145 150

<210> 197
<211> 4842
<212> DNA
<213> Homo sapiens

<400> 197

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ggggtcggcg ccgccgtgcg cgcgcgcctg gcgctggcct tggcgctggc 150
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ccttccagaa ttgcttttcc agagcacgcc gaagctcacc agactagatt 500
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<210> 198
 <211> 1523
 <212> PRT
 <213> Homo sapiens

<400> 198
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 Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val
 35 40 45
 Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro
 50 55 60
 Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg
 65 70 75
 Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu
 80 85 90
 His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe
 95 100 105
 Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys
 110 115 120
 Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu
 125 130 135
 Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg
 140 145 150
 Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp
 155 160 165

Asn Asn His Ile	Ser Cys Ile Glu Asp	Gly Ala Phe Arg Ala	Leu
170		175	180
Arg Asp Leu Glu	Ile Leu Thr Leu Asn	Asn Asn Asn Ile Ser	Arg
185		190	195
Ile Leu Val Thr	Ser Phe Asn His Met	Pro Lys Ile Arg Thr	Leu
200		205	210
Arg Leu His Ser	Asn His Leu Tyr Cys	Asp Cys His Leu Ala	Trp
215		220	225
Leu Ser Asp Trp	Leu Arg Gln Arg Arg	Thr Val Gly Gln Phe	Thr
230		235	240
Leu Cys Met Ala	Pro Val His Leu Arg	Gly Phe Asn Val Ala	Asp
245		250	255
Val Gln Lys Lys	Glu Tyr Val Cys Pro	Ala Pro His Ser Glu	Pro
260		265	270
Pro Ser Cys Asn	Ala Asn Ser Ile Ser	Cys Pro Ser Pro Cys	Thr
275		280	285
Cys Ser Asn Asn	Ile Val Asp Cys Arg	Gly Lys Gly Leu Met	Glu
290		295	300
Ile Pro Ala Asn	Leu Pro Glu Gly Ile	Val Glu Ile Arg Leu	Glu
305		310	315
Gln Asn Ser Ile	Lys Ala Ile Pro Ala	Gly Ala Phe Thr Gln	Tyr
320		325	330
Lys Lys Leu Lys	Arg Ile Asp Ile Ser	Lys Asn Gln Ile Ser	Asp
335		340	345
Ile Ala Pro Asp	Ala Phe Gln Gly Leu	Lys Ser Leu Thr Ser	Leu
350		355	360
Val Leu Tyr Gly	Asn Lys Ile Thr Glu	Ile Ala Lys Gly Leu	Phe
365		370	375
Asp Gly Leu Val	Ser Leu Gln Leu Leu	Leu Leu Asn Ala Asn	Lys
380		385	390
Ile Asn Cys Leu	Arg Val Asn Thr Phe	Gln Asp Leu Gln Asn	Leu
395		400	405
Asn Leu Leu Ser	Leu Tyr Asp Asn Lys	Leu Gln Thr Ile Ser	Lys
410		415	420
Gly Leu Phe Ala	Pro Leu Gln Ser Ile	Gln Thr Leu His Leu	Ala
425		430	435
Gln Asn Pro Phe	Val Cys Asp Cys His	Leu Lys Trp Leu Ala	Asp
440		445	450
Tyr Leu Gln Asp	Asn Pro Ile Glu Thr	Ser Gly Ala Arg Cys	Ser

				455					460					465
Ser	Pro	Arg	Arg	Leu 470	Ala	Asn	Lys	Arg	Ile 475	Ser	Gln	Ile	Lys	Ser 480
Lys	Lys	Phe	Arg	Cys 485	Ser	Gly	Ser	Glu	Asp 490	Tyr	Arg	Ser	Arg	Phe 495
Ser	Ser	Glu	Cys	Phe 500	Met	Asp	Leu	Val	Cys 505	Pro	Glu	Lys	Cys	Arg 510
Cys	Glu	Gly	Thr	Ile 515	Val	Asp	Cys	Ser	Asn 520	Gln	Lys	Leu	Val	Arg 525
Ile	Pro	Ser	His	Leu 530	Pro	Glu	Tyr	Val	Thr 535	Asp	Leu	Arg	Leu	Asn 540
Asp	Asn	Glu	Val	Ser 545	Val	Leu	Glu	Ala	Thr 550	Gly	Ile	Phe	Lys	Lys 555
Leu	Pro	Asn	Leu	Arg 560	Lys	Ile	Asn	Leu	Ser 565	Asn	Asn	Lys	Ile	Lys 570
Glu	Val	Arg	Glu	Gly 575	Ala	Phe	Asp	Gly	Ala 580	Ala	Ser	Val	Gln	Glu 585
Leu	Met	Leu	Thr	Gly 590	Asn	Gln	Leu	Glu	Thr 595	Val	His	Gly	Arg	Val 600
Phe	Arg	Gly	Leu	Ser 605	Gly	Leu	Lys	Thr	Leu 610	Met	Leu	Arg	Ser	Asn 615
Leu	Ile	Ser	Cys	Val 620	Ser	Asn	Asp	Thr	Phe 625	Ala	Gly	Leu	Ser	Ser 630
Val	Arg	Leu	Leu	Ser 635	Leu	Tyr	Asp	Asn	Arg 640	Ile	Thr	Thr	Ile	Thr 645
Pro	Gly	Ala	Phe	Thr 650	Thr	Leu	Val	Ser	Leu 655	Ser	Thr	Ile	Asn	Leu 660
Leu	Ser	Asn	Pro	Phe 665	Asn	Cys	Asn	Cys	His 670	Leu	Ala	Trp	Leu	Gly 675
Lys	Trp	Leu	Arg	Lys 680	Arg	Arg	Ile	Val	Ser 685	Gly	Asn	Pro	Arg	Cys 690
Gln	Lys	Pro	Phe	Phe 695	Leu	Lys	Glu	Ile	Pro 700	Ile	Gln	Asp	Val	Ala 705
Ile	Gln	Asp	Phe	Thr 710	Cys	Asp	Gly	Asn	Glu 715	Glu	Ser	Ser	Cys	Gln 720
Leu	Ser	Pro	Arg	Cys 725	Pro	Glu	Gln	Cys	Thr 730	Cys	Met	Glu	Thr	Val 735
Val	Arg	Cys	Ser	Asn 740	Lys	Gly	Leu	Arg	Ala 745	Leu	Pro	Arg	Gly	Met 750

Pro	Lys	Asp	Val	Thr 755	Glu	Leu	Tyr	Leu	Glu 760	Gly	Asn	His	Leu	Thr 765
Ala	Val	Pro	Arg	Glu 770	Leu	Ser	Ala	Leu	Arg 775	His	Leu	Thr	Leu	Ile 780
Asp	Leu	Ser	Asn	Asn 785	Ser	Ile	Ser	Met	Leu 790	Thr	Asn	Tyr	Thr	Phe 795
Ser	Asn	Met	Ser	His 800	Leu	Ser	Thr	Leu	Ile 805	Leu	Ser	Tyr	Asn	Arg 810
Leu	Arg	Cys	Ile	Pro 815	Val	His	Ala	Phe	Asn 820	Gly	Leu	Arg	Ser	Leu 825
Arg	Val	Leu	Thr	Leu 830	His	Gly	Asn	Asp	Ile 835	Ser	Ser	Val	Pro	Glu 840
Gly	Ser	Phe	Asn	Asp 845	Leu	Thr	Ser	Leu	Ser 850	His	Leu	Ala	Leu	Gly 855
Thr	Asn	Pro	Leu	His 860	Cys	Asp	Cys	Ser	Leu 865	Arg	Trp	Leu	Ser	Glu 870
Trp	Val	Lys	Ala	Gly 875	Tyr	Lys	Glu	Pro	Gly 880	Ile	Ala	Arg	Cys	Ser 885
Ser	Pro	Glu	Pro	Met 890	Ala	Asp	Arg	Leu	Leu 895	Leu	Thr	Thr	Pro	Thr 900
His	Arg	Phe	Gln	Cys 905	Lys	Gly	Pro	Val	Asp 910	Ile	Asn	Ile	Val	Ala 915
Lys	Cys	Asn	Ala	Cys 920	Leu	Ser	Ser	Pro	Cys 925	Lys	Asn	Asn	Gly	Thr 930
Cys	Thr	Gln	Asp	Pro 935	Val	Glu	Leu	Tyr	Arg 940	Cys	Ala	Cys	Pro	Tyr 945
Ser	Tyr	Lys	Gly	Lys 950	Asp	Cys	Thr	Val	Pro 955	Ile	Asn	Thr	Cys	Ile 960
Gln	Asn	Pro	Cys	Gln 965	His	Gly	Gly	Thr	Cys 970	His	Leu	Ser	Asp	Ser 975
His	Lys	Asp	Gly	Phe 980	Ser	Cys	Ser	Cys	Pro 985	Leu	Gly	Phe	Glu	Gly 990
Gln	Arg	Cys	Glu	Ile 995	Asn	Pro	Asp	Asp	Cys 1000	Glu	Asp	Asn	Asp	Cys 1005
Glu	Asn	Asn	Ala	Thr 1010	Cys	Val	Asp	Gly	Ile 1015	Asn	Asn	Tyr	Val	Cys 1020
Ile	Cys	Pro	Pro	Asn 1025	Tyr	Thr	Gly	Glu	Leu 1030	Cys	Asp	Glu	Val	Ile 1035
Asp	His	Cys	Val	Pro	Glu	Leu	Asn	Leu	Cys	Gln	His	Glu	Ala	Lys

Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly	1040	1045	1050
1055	1060	1065	
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala	1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly	1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu	1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln	1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu	1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu	1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu	1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln	1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp	1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu	1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val	1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr	1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys	1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser	1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala	1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys	1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala	1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys	1325	1330	1335

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser
1340 1345 1350

Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp
1355 1360 1365

Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly
1370 1375 1380

Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
1385 1390 1395

Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn
1400 1405 1410

Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
1415 1420 1425

Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly
1430 1435 1440

Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg
1445 1450 1455

Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala
1460 1465 1470

Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln
1475 1480 1485

Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
1490 1495 1500

Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu
1505 1510 1515

Glu Cys Gly Cys Leu Ala Cys Ser
1520

<210> 199
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 199
atggagattc ctgccaaactt gccg 24

<210> 200
<211> 24
<212> DNA
<213> Artificial

<220>

<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 200
ttgttgcat tgaggaggag cagc 24

<210> 201
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 201
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202
<211> 753
<212> DNA
<213> Homo sapiens

<400> 202
ggatgcagga cgctccctg agctgcctgt caccgactag gtggagcagt 50
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gaatctgcct ttccagttct gtctccggca ggctttgagg atgaaggctg 150
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250
caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300
agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350
gactatggca tcttcagat caacagcttc gcgtggtgca gacgcggaaa 400
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450
atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500
caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550
cctgtccgag tggaaaaaag gctgtgaggt ttcctaaact ggaactggac 600
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cctgtgtcat cttgtcccg ttcctcccaa tttccttctt caaacttgga 700
gagggaaaat taagctatac ttttaagaaa ataaatattt ccattttaat 750
gtc 753

<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 203
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 1 5 10 15
 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile
 20 25 30
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
 35 40 45
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
 50 55 60
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
 65 70 75
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
 80 85 90
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
 95 100 105
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
 110 115 120
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
 125 130 135
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
 140 145

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 204
 gcaggctttg aggatgaagg ctgc 24

<210> 205
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.'

<400> 205
ctcattggct gcctgggtcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 207
tcagtgaacca aggtgagca ggcg 24

<210> 208
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 208
ctacactcgt tgcaaaactgg caaaaatatt ctcgagggct ggcctgg 47

<210> 209
<211> 1648
<212> DNA
<213> Homo sapiens

<400> 209
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cctcagcagt gtcattgtgt aaaaacgcca agctgaatat atcatgcccc 100
tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150
ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
gcggaagaag atcctatatt actgtcactt cccagatctg cttctcacca 250


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agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300
gaggaataca ccacaggcat ggcagactgc atcttagtca acagccagtt 350
cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400
ctgatgtcct ctatccatct ctaaattgtca ccagctttga ctcagttgtt 450
cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgctgct 500
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acattatcag gaattgaaga aaatgggtcca acagtccgac cttggccagt 700
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tgtcattcca tgttcagcag agtattttaa ttatattttc tcgggattat 1350
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atagtttaag tgtgtatcat tatcaaagtt gattaatttg gcttcatagt 1450
ataatgagag cagggctatt gtagttcca gattcaatcc accgaagtgt 1500
tactgtcat ctgtaggga atttttgttt gtccctgtctt tgccctggatc 1550
catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600
actgagatat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaaaa 1648

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<210> 210
<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

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Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly
 1          5          10          15
Glu Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val
          20          25          30
Phe Arg Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His
          35          40          45
Phe Pro Asp Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg
          50          55          60
Leu Tyr Arg Ala Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly
          65          70          75
Met Ala Asp Cys Ile Leu Val Asn Ser Gln Phe Thr Ala Ala Val
          80          85          90
Phe Lys Glu Thr Phe Lys Ser Leu Ser His Ile Asp Pro Asp Val
          95          100          105
Leu Tyr Pro Ser Leu Asn Val Thr Ser Phe Asp Ser Val Val Pro
          110          115          120
Glu Lys Leu Asp Asp Leu Val Pro Lys Gly Lys Lys Phe Leu Leu
          125          130          135
Leu Ser Ile Asn Arg Tyr Glu Arg Lys Lys Asn Leu Thr Leu Ala
          140          145          150
Leu Glu Ala Leu Val Gln Leu Arg Gly Arg Leu Thr Ser Gln Asp
          155          160          165
Trp Glu Arg Val His Leu Ile Val Ala Gly Gly Tyr Asp Glu Arg
          170          175          180
Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys Lys Met Val
          185          190          195
Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg Ser Phe
          200          205          210
Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys Val
          215          220          225
Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu
          230          235          240
Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly
          245          250          255
Pro Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu
          260          265          270

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ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050
gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100
tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150
tgggtacttca ggatcctaata acttggccat ctccacacaa gtttgatcca 1200
gatcggtttg atgatgaatt agtaatgaaa actttttcct cacttggtgatt 1250
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agcttggtatc actgtctcaa agagatatta aaattttata catttaaaat 1450
cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500
aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550
ttaa 1554

<210> 212
<211> 462
<212> PRT
<213> Homo sapiens

<400> 212
Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu
1 5 10 15
Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala
20 25 30
Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu
35 40 45
Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn
50 55 60
Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg
65 70 75
Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His
80 85 90
Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys
95 100 105
Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn
110 115 120
His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu
125 130 135
Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu

Asp Lys Trp Leu Ser Tyr Pro Glu Thr	Gln His Val Pro Leu Ser
155	160 165
Gln His Met Leu Gly Phe Ala Met Lys	Ser Val Thr Gln Met Val
170	175 180
Met Gly Ser Thr Phe Glu Asp Asp Gln	Glu Val Ile Arg Phe Gln
185	190 195
Lys Asn His Gly Thr Val Trp Ser Glu	Ile Gly Lys Gly Phe Leu
200	205 210
Asp Gly Ser Leu Asp Lys Asn Met Thr	Arg Lys Lys Gln Tyr Glu
215	220 225
Asp Ala Leu Met Gln Leu Glu Ser Val	Leu Arg Asn Ile Ile Lys
230	235 240
Glu Arg Lys Gly Arg Asn Phe Ser Gln	His Ile Phe Ile Asp Ser
245	250 255
Leu Val Gln Gly Asn Leu Asn Asp Gln	Gln Ile Leu Glu Asp Ser
260	265 270
Met Ile Phe Ser Leu Ala Ser Cys Ile	Ile Thr Ala Lys Leu Cys
275	280 285
Thr Trp Ala Ile Cys Phe Leu Thr Thr	Ser Glu Glu Val Gln Lys
290	295 300
Lys Leu Tyr Glu Glu Ile Asn Gln Val	Phe Gly Asn Gly Pro Val
305	310 315
Thr Pro Glu Lys Ile Glu Gln Leu Arg	Tyr Cys Gln His Val Leu
320	325 330
Cys Glu Thr Val Arg Thr Ala Lys Leu	Thr Pro Val Ser Ala Gln
335	340 345
Leu Gln Asp Ile Glu Gly Lys Ile Asp	Arg Phe Ile Ile Pro Arg
350	355 360
Glu Thr Leu Val Leu Tyr Ala Leu Gly	Val Val Leu Gln Asp Pro
365	370 375
Asn Thr Trp Pro Ser Pro His Lys Phe	Asp Pro Asp Arg Phe Asp
380	385 390
Asp Glu Leu Val Met Lys Thr Phe Ser	Ser Leu Gly Phe Ser Gly
395	400 405
Thr Gln Glu Cys Pro Glu Leu Arg Phe	Ala Tyr Met Val Thr Thr
410	415 420
Val Leu Leu Ser Val Leu Val Lys Arg	Leu His Leu Leu Ser Val
425	430 435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
455 460

<210> 213
<211> 759
<212> DNA
<213> Homo sapiens

<400> 213
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tccagcctca gagaccgccg cccttggtccc cgagggccat gggccgggtc 100
tcagggcttg tgccctctcg ctctctgacg ctctggcgcg atctggtggt 150
cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200
ctctcacgtt caccctcgag gagtatgaca agcaggacat tcagctggtg 250
gccgcgtct ctgtcacctt gggcctcttt gcagtggagc tggccggttt 300
cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
gggctcactg tagtgcattc gtggccctgt ccttcttcat attcgagcgt 400
tgaggagtga ctacgtattg gtacattttt gtcttctgca gtgcccttcc 450
agctgtcact gaaatggctt ttttcgtcac cgtctttggg ctgaaaaaga 500
aaccttcttg attaccttca tgacgggaac ctaaggacga agcctacagg 550
ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600
ttccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650
tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700
tgttttgtag taacattaag acttatatac agtttttaggg gacaattaaa 750
aaaaaaaaa 759

<210> 214
<211> 140
<212> PRT
<213> Homo sapiens

<400> 214
Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
1 5 10 15
Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
20 25 30
Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
35 40 45

Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
50 55 60
Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
65 70 75
Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
80 85 90
Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
95 100 105
Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
110 115 120
Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
125 130 135
Lys Lys Lys Pro Phe
140

<210> 215
<211> 697
<212> DNA
<213> Homo sapiens

<400> 215
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cctgggctct cccagcctc cttcgactcg gagcgggtca ggagacagaa 100
gaccggcct gctgcagccc catagtgcc cggaacgagt ggaaggccct 150
ggcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200
tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250
caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300
cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450
ccaggccatc cgggcagccc aggtctact ggctgcggt gtggctcagg 500
gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550
acactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600
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catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216
<211> 196
<212> PRT

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tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc 300
cccaaccgcc cgaaccacag cccccaccc tcagccaagg tgaagaaaat 350
ctttggctgg ggcgacttct actccaacat caagacggtg gccctgaacc 400
tgctcgtcac aggggaagatt gtggaccatg gcaatgggac cttcagcgtc 450
caattccaac acaatgccac agggcaggga aacatctcca tcagcctcgt 500
gccccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg 550
aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600
gaacggggcc gccggacctc gctttgcacc cacgaccag ccaagatctg 650
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[illegible]

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<210> 218
<211> 252
<212> PRT
<213> Homo sapiens
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<400> 218														
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Glu	Asp	Pro	Glu	Arg 35	Asp	Asp	His	Glu	Gly 40	Gln	Pro	Arg	Pro	Arg 45
Val	Pro	Arg	Lys	Arg 50	Gly	His	Ile	Ser	Pro 55	Lys	Ser	Arg	Pro	Met 60
Ala	Asn	Ser	Thr	Leu 65	Leu	Gly	Leu	Leu	Ala 70	Pro	Pro	Gly	Glu	Ala 75
Trp	Gly	Ile	Leu	Gly 80	Gln	Pro	Pro	Asn	Arg 85	Pro	Asn	His	Ser	Pro 90
Pro	Pro	Ser	Ala	Lys 95	Val	Lys	Lys	Ile	Phe 100	Gly	Trp	Gly	Asp	Phe 105
Tyr	Ser	Asn	Ile	Lys 110	Thr	Val	Ala	Leu	Asn 115	Leu	Leu	Val	Thr	Gly 120
Lys	Ile	Val	Asp	His 125	Gly	Asn	Gly	Thr	Phe 130	Ser	Val	His	Phe	Gln 135
His	Asn	Ala	Thr	Gly 140	Gln	Gly	Asn	Ile	Ser 145	Ile	Ser	Leu	Val	Pro 150
Pro	Ser	Lys	Ala	Val 155	Glu	Phe	His	Gln	Glu 160	Gln	Gln	Ile	Phe	Ile 165
Glu	Ala	Lys	Ala	Ser 170	Lys	Ile	Phe	Asn	Cys 175	Arg	Met	Glu	Trp	Glu 180
Lys	Val	Glu	Arg	Gly 185	Arg	Arg	Thr	Ser	Leu 190	Cys	Thr	His	Asp	Pro 195
Ala	Lys	Ile	Cys	Ser 200	Arg	Asp	His	Ala	Gln 205	Ser	Ser	Ala	Thr	Trp 210

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
245 250

<210> 219
<211> 2065
<212> DNA
<213> Homo sapiens

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agctcgaggg gagactttga cttcaagcca cagaattggt ggaagtgtgc 200
gcgccgcccgc cgccgtcgct cctgcagcgc tgctcgacct gcccgtagca 250
tcttcccagag caccgggatc ccggggtagg aggcgacgcg ggcgagcacc 300
agcgccagcc ggctgcggct gccacacagg ctcaccatgg gctccgggcg 350
ccgggcgctg tccgcggtgc cggccgtgct gctggtcctc acgctgccgg 400
ggctgcccgct ctgggcacag aacgacacgg agcccatcgt gctggagggc 450
aagtgtctgg tgggtgtgca ctcgaacccg gccacggact ccaagggctc 500
ctcttctctc ccgctgggga tatcggtccg ggcgccaac tccaaggtcg 550
ccttctcggc ggtgcggagc accaaccacg agccatccga gatgagcaac 600
aagacgcgca tcatttactt cgatcagatc ctggtgaatg tgggtaattt 650
tttcacattg gagtctgtct ttgtagcacc aagaaaagga atttacagtt 700
tcagttttca cgtgattaaa gtctaccaga gccaaactat ccaggttaac 750
ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaga 800
tggtactcgt gaagctgcc acaatggtgt cctgctctac ctagataaag 850
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cagtattcca cgttttcttg ctttctggtg ttccccctat aggattcaat 950
ttctccatga tgttcatcca ggtgagggat gaccactcc tgagttattg 1000
gaagatcatt ttttcatcat tggattgatg ttttttattg gtttctcatg 1050
ggtggatatg gattctaagg attctagcct gtctgaacca atacaaaatt 1100

tcacagatta tttgtgtgtg tctgtttcag tatatttgga ttgggactct 1150
aagcagataa tacctatgct taaatgtaac agtcaaaagc tgtctgcaag 1200
acttattctg aatttcattt cctgggatta ctgaattagt tacagatgtg 1250
gaattttatt tgtttagttt taaaagactg gcaaccaggt ctaaggatta 1300
gaaaactcta aagttctgac ttcaatcaac ggtagtgtg atactgccaa 1350
agaactgtat actgtgttaa tatattgatt atatttgatt ttattccttt 1400
ggaattagtt tgtttggttc ttgtaaaaaa ctgggatttt ttttttcagt 1450
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aaatttacct tgactacgat atcatcgaca tgacttctct caaaaaaaaa 1550
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Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu
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Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	
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Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	
				80					85					90	
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	
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Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	
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Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	
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Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	
				140					145					150	
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	
				155					160					165	
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu	
				170					175					180	
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly	
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 <211> 24
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-24
 <223> Synthetic construct.

<400> 222
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<210> 223
 <211> 40

<212> DNA
<213> Artificial

<220>
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<222> 1-40
<223> Synthetic construct.

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<211> 902
<212> DNA
<213> Homo sapiens

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<211> 257
<212> PRT

<213> Homo sapiens

<400> 225

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Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile		50		55		60		
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly		65		70		75		
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr		80		85		90		
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn		95		100		105		
Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser		110		115		120		
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Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly		140		145		150		
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val		155		160		165		
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly		170		175		180		
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr		185		190		195		
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly		200		205		210		
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr		215		220		225		
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu		230		235		240		
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Ser Arg

<210> 226

<211> 3939

<212> DNA

<213> Homo sapiens

<400> 226

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<212> PRT
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<400> 227
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 35 40 45
 Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn
 50 55 60
 Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys Gln
 65 70 75
 Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val
 80 85 90
 Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg
 95 100 105
 Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro
 110 115 120
 Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser
 125 130 135
 Thr Leu Ser Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg
 140 145 150
 Met Asp Asp Phe Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn
 155 160 165
 Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu
 170 175 180
 Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn Lys Ala Phe
 185 190 195
 Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro Val Tyr
 200 205 210
 Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr Met
 215 220 225
 Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
 230 235 240
 Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala
 245 250 255
 Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro
 260 265 270
 Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser
 275 280 285
 Gln Ala Val Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys
 290 295 300
 Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala
 305 310 315
 Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala

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Asp	Ser	Phe	Pro	Gly	Ser	Ser	Pro	Tyr	Glu	Gly	Tyr	Asn	Tyr	Gly
				350					355					360
Ser	Phe	Glu	Asn	Val	Ser	Gly	Ser	Thr	Asp	Gly	Leu	Val	Asp	Ser
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Ala	Gly	Thr	Gly	Asp	Leu	Ser	Tyr	Gly	Tyr	Gln	Gly	Arg	Ser	Phe
				380					385					390
Glu	Pro	Val	Gly	Thr	Arg	Pro	Arg	Val	Asp	Ser	Met	Ser	Ser	Val
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Glu	Glu	Asp	Asp	Tyr	Asp	Thr	Leu	Thr	Asp	Ile	Asp	Ser	Asp	Lys
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Asn	Val	Ile	Arg	Thr	Lys	Gln	Tyr	Leu	Tyr	Val	Ala	Asp	Leu	Ala
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Arg	Lys	Asp	Lys	Arg	Val	Leu	Arg	Lys	Lys	Tyr	Gln	Ile	Tyr	Phe
				440					445					450
Trp	Asn	Ile	Ala	Thr	Ile	Ala	Val	Phe	Tyr	Ala	Leu	Pro	Val	Val
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Gln	Leu	Val	Ile	Thr	Tyr	Gln	Thr	Val	Val	Asn	Val	Thr	Gly	Asn
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Gln	Asp	Ile	Cys	Tyr	Tyr	Asn	Phe	Leu	Cys	Ala	His	Pro	Leu	Gly
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Leu	Leu	Gly	Leu	Leu	Phe	Leu	Leu	Ile	Ile	Leu	Gln	Arg	Glu	Ile
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Ala	Leu	Met	Met	Glu	Gly	Leu	Leu	Ser	Ala	Cys	Tyr	His	Val	Cys
				560					565					570
Pro	Asn	Tyr	Thr	Asn	Phe	Gln	Phe	Asp	Thr	Ser	Phe	Met	Tyr	Met
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Ile	Ala	Gly	Leu	Cys	Met	Leu	Lys	Leu	Tyr	Gln	Lys	Arg	His	Pro
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Val	Ile	Phe	Phe	Ser	Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn	
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Thr	Ala	Phe	Trp	Ile	Val	Phe	Ser	Ile	Ile	His	Ile	Ile	Ala	Thr	
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Leu	Leu	Leu	Ser	Thr	Gln	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu	
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His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser	
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 <211> 2848
 <212> DNA
 <213> Homo sapiens

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 cctccctgag gatgtggagc ccgggactct ggtggccatg ctaacagcca 1550
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 aggggagaca cagaagggac ttttggcctg gattgggagc cagactctgg 1650

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gcgcccagcc	tggggacacc	tacacggtgc	ttgtggaggc	ccaggataca	2050
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<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

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Ala Leu Pro Lys Ala Gln Pro Ala Glu Leu Ser Val Glu Val Pro

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Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp
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Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser
				65					70					75
Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala
				80					85					90
Glu	Tyr	Gln	Leu	Gln	Val	Thr	Leu	Glu	Met	Gln	Asp	Gly	His	Val
				95					100					105
Leu	Trp	Gly	Pro	Gln	Pro	Val	Leu	Val	His	Val	Lys	Asp	Glu	Asn
				110					115					120
Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu
				125					130					135
Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala
				140					145					150
Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe
				155					160					165
His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe
				170					175					180
Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly
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Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu
				200					205					210
Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala
				215					220					225
Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser
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Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro
				245					250					255
His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr
				260					265					270
His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu
				275					280					285
Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala
				290					295					300
Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp
				305					310					315

Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn	
				320					325					330	
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile	
				335					340					345	
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala	
				350					355					360	
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr	
				365					370					375	
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala	
				380					385					390	
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu	
				395					400					405	
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met	
				410					415					420	
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val	
				425					430					435	
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile	
				440					445					450	
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro	
				455					460					465	
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu	
				470					475					480	
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr	
				485					490					495	
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val	
				500					505					510	
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser	
				515					520					525	
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly	
				530					535					540	
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val	
				545					550					555	
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu	
				560					565					570	
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr	
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Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu	
				590					595					600	
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly	

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Glu	Val	His	Thr	Ala	Gln	Ser	Leu	Gln	Gly	Ala	Gln	Pro	Gly	Asp
				620					625					630
Thr	Tyr	Thr	Val	Leu	Val	Glu	Ala	Gln	Asp	Thr	Ala	Leu	Thr	Leu
				635					640					645
Ala	Pro	Val	Pro	Ser	Gln	Tyr	Leu	Cys	Thr	Pro	Arg	Gln	Asp	His
				650					655					660
Gly	Leu	Ile	Val	Ser	Gly	Pro	Ser	Lys	Asp	Pro	Asp	Leu	Ala	Ser
				665					670					675
Gly	His	Gly	Pro	Tyr	Ser	Phe	Thr	Leu	Gly	Pro	Asn	Pro	Thr	Val
				680					685					690
Gln	Arg	Asp	Trp	Arg	Leu	Gln	Thr	Leu	Asn	Gly	Ser	His	Ala	Tyr
				695					700					705
Leu	Thr	Leu	Ala	Leu	His	Trp	Val	Glu	Pro	Arg	Glu	His	Ile	Ile
				710					715					720
Pro	Val	Val	Val	Ser	His	Asn	Ala	Gln	Met	Trp	Gln	Leu	Leu	Val
				725					730					735
Arg	Val	Ile	Val	Cys	Arg	Cys	Asn	Val	Glu	Gly	Gln	Cys	Met	Arg
				740					745					750
Lys	Val	Gly	Arg	Met	Lys	Gly	Met	Pro	Thr	Lys	Leu	Ser	Ala	Val
				755					760					765
Gly	Ile	Leu	Val	Gly	Thr	Leu	Val	Ala	Ile	Gly	Ile	Phe	Leu	Ile
				770					775					780
Leu	Ile	Phe	Thr	His	Trp	Thr	Met	Ser	Arg	Lys	Lys	Asp	Pro	Asp
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Gln	Pro	Ala	Asp	Ser	Val	Pro	Leu	Lys	Ala	Thr	Val			
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<210> 230
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 230
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<210> 231
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Artificial Sequence
 <222> full
 <223> Synthetic oligonucleotide probe

<400> 231
 cctgagctgt aacccactc cagg 24

<210> 232
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 232
 agagtctgtc ccagctatct tgt 23

<210> 233
 <211> 2786
 <212> DNA
 <213> Homo sapiens

<400> 233
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 cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150
 acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200
 gatgtcctgg tcccatctgt cagtctgcag gcatttaaact ccttcctgag 250
 atcccagggc ttagagtacg cagtgcacat tgaggacctg caggcccttt 300
 tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350
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 agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500
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ttactcctct cttccctttg ttattcagtg tgaccaggat ggcgggaggg 2250
gatctgtgtc actgtaggta ctgtgccag gaaggctggg tgaagtgacc 2300

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<210> 234
<211> 421
<212> PRT
<213> Homo sapiens
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<400> 234
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Cys Gly Gln Glu Lys Phe Phe Gly Asp Gln Val Leu Arg Ile Asn
          20          25          30
Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn
          35          40          45
Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe
          50          55          60
Asn Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala
          65          70          75
Phe Lys Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr
          80          85          90
Ile Glu Asp Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met
          95          100          105
Gln His Asn Glu Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr
          110          115          120
Gly Ala Tyr His Ser Leu Glu Ala Ile Tyr His Glu Met Asp Asn
          125          130          135
Ile Ala Ala Asp Phe Pro Asp Leu Ala Arg Arg Val Lys Ile Gly
          140          145          150
His Ser Phe Glu Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr
          155          160          165

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Gly	Lys	Gly	Val	Arg 170	Arg	Pro	Ala	Val	Trp 175	Leu	Asn	Ala	Gly	Ile 180
His	Ser	Arg	Glu	Trp 185	Ile	Ser	Gln	Ala	Thr 190	Ala	Ile	Trp	Thr	Ala 195
Arg	Lys	Ile	Val	Ser 200	Asp	Tyr	Gln	Arg	Asp 205	Pro	Ala	Ile	Thr	Ser 210
Ile	Leu	Glu	Lys	Met 215	Asp	Ile	Phe	Leu	Leu 220	Pro	Val	Ala	Asn	Pro 225
Asp	Gly	Tyr	Val	Tyr 230	Thr	Gln	Thr	Gln	Asn 235	Arg	Leu	Trp	Arg	Lys 240
Thr	Arg	Ser	Arg	Asn 245	Pro	Gly	Ser	Ser	Cys 250	Ile	Gly	Ala	Asp	Pro 255
Asn	Arg	Asn	Trp	Asn 260	Ala	Ser	Phe	Ala	Gly 265	Lys	Gly	Ala	Ser	Asp 270
Asn	Pro	Cys	Ser	Glu 275	Val	Tyr	His	Gly	Pro 280	His	Ala	Asn	Ser	Glu 285
Val	Glu	Val	Lys	Ser 290	Val	Val	Asp	Phe	Ile 295	Gln	Lys	His	Gly	Asn 300
Phe	Lys	Gly	Phe	Ile 305	Asp	Leu	His	Ser	Tyr 310	Ser	Gln	Leu	Leu	Met 315
Tyr	Pro	Tyr	Gly	Tyr 320	Ser	Val	Lys	Lys	Ala 325	Pro	Asp	Ala	Glu	Glu 330
Leu	Asp	Lys	Val	Ala 335	Arg	Leu	Ala	Ala	Lys 340	Ala	Leu	Ala	Ser	Val 345
Ser	Gly	Thr	Glu	Tyr 350	Gln	Val	Gly	Pro	Thr 355	Cys	Thr	Thr	Val	Tyr 360
Pro	Ala	Ser	Gly	Ser 365	Ser	Ile	Asp	Trp	Ala 370	Tyr	Asp	Asn	Gly	Ile 375
Lys	Phe	Ala	Phe	Thr 380	Phe	Glu	Leu	Arg	Asp 385	Thr	Gly	Thr	Tyr	Gly 390
Phe	Leu	Leu	Pro	Ala 395	Asn	Gln	Ile	Ile	Pro 400	Thr	Ala	Glu	Glu	Thr 405
Trp	Leu	Gly	Leu	Lys 410	Thr	Ile	Met	Glu	His 415	Val	Arg	Asp	Asn	Leu 420

Tyr

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<210> 235
<211> 1743
<212> DNA
<213> Homo sapiens
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cccgcccttc ctccacaaag agcacccttg cctcacaggt gtattccctc 200
aacaccgact ttgccttccg cctataccgc aggctggttt tggagacccc 250
gagtcagaac atctttcttct cccctgtgag tgtctccact tccctggcca 300
tgctctccct tggggcccac tcagtcacca agaccagat tctccagggc 350
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Lys	Trp	Glu	Lys	Pro	Phe	His	Leu	Glu	Tyr	Thr	Arg	Lys	Asn	Phe
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Pro	Phe	Leu	Val	Gly	Glu	Gln	Val	Thr	Val	Gln	Val	Pro	Met	Met
				230					235					240
His	Gln	Lys	Glu	Gln	Phe	Ala	Phe	Gly	Val	Asp	Thr	Glu	Leu	Asn
				245					250					255
Cys	Phe	Val	Leu	Gln	Met	Asp	Tyr	Lys	Gly	Asp	Ala	Val	Ala	Phe
				260					265					270
Phe	Val	Leu	Pro	Ser	Lys	Gly	Lys	Met	Arg	Gln	Leu	Glu	Gln	Ala
				275					280					285
Leu	Ser	Ala	Arg	Thr	Leu	Ile	Lys	Trp	Ser	His	Ser	Leu	Gln	Lys
				290					295					300
Arg	Trp	Ile	Glu	Val	Phe	Ile	Pro	Arg	Phe	Ser	Ile	Ser	Ala	Ser
				305					310					315
Tyr	Asn	Leu	Glu	Thr	Ile	Leu	Pro	Lys	Met	Gly	Ile	Gln	Asn	Ala
				320					325					330
Phe	Asp	Lys	Asn	Ala	Asp	Phe	Ser	Gly	Ile	Ala	Lys	Arg	Asp	Ser
				335					340					345
Leu	Gln	Val	Ser	Lys	Ala	Thr	His	Lys	Ala	Val	Leu	Asp	Val	Ser
				350					355					360
Glu	Glu	Gly	Thr	Glu	Ala	Thr	Ala	Ala	Thr	Thr	Thr	Lys	Phe	Ile
				365					370					375
Val	Arg	Ser	Lys	Asp	Gly	Pro	Ser	Tyr	Phe	Thr	Val	Ser	Phe	Asn
				380					385					390
Arg	Thr	Phe	Leu	Met	Met	Ile	Thr	Asn	Lys	Ala	Thr	Asp	Gly	Ile
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Leu	Phe	Leu	Gly	Lys	Val	Glu	Asn	Pro	Thr	Lys	Ser			
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<210> 237

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<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

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<210> 238

<211> 47
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-47
 <223> Synthetic construct.

 <400> 238
 ctttgcctgtt ggctctgtg ctccaacca tgcaaggaca gggcagg 47

 <210> 239
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 239
 tgactcgggg tctccaaaac cagc 24

 <210> 240
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 240
 ggtataggcg gaaggcaaag tcgg 24

 <210> 241
 <211> 48
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-48
 <223> Synthetic construct.

 <400> 241
 ggcatttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

 <210> 242
 <211> 2436
 <212> DNA
 <213> Homo sapiens

 <400> 242
 ggctgaccgt gctacattgc ctggaggaag cctaaggaaac ccaggcatcc 50

agctgcccac gcttgagtc aagatttttc ccaggaacac aaacgtagga 100
gacccacgct cctggaagca ccagccttta tctcttcacc ttcaagtccc 150
ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta 200
ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250
aaaggaaatg ttctccttat gtttgggtcta ctattgcatt tagaagctgc 300
aacaatttcc aatgagacta gcacctctgc caactctgga tccagtgtga 350
tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc 400
agtgggggtca gcacagccac catctcaggg tccagcgtga cctccaatgg 450
ggtcagcata gtcaccaact ctgagttcca tacaacctcc agtgggatca 500
gcacagccac caactctgag ttcagcacag cgtccagtgg gatcagcata 550
gccaccaact ctgagtccag cacaacctcc agtggggcca gcacagccac 600
caactctgag tccagcacac cctccagtgg ggccagcaca gtcaccaact 650
ctgggtccag tgtgacctcc agtggagcca gactgccac caactctgag 700
tccagcacag tgtccagtag ggccagcact gccaccaact ctgagtctag 750
cacactctcc agtggggcca gcacagccac caactctgac tccagcaca 800
cctccagtgg ggctagcaca gccaccaact ctgagtccag cacaacctcc 850
agtggggcca gcacagccac caactctgag tccagcacag tgtccagtag 900
ggccagcact gccaccaact ctgagtccag cacaacctcc agtggggcca 950
gcacagccac caactctgag tccagaacga cctccaatgg ggctggcaca 1000
gccaccaact ctgagtccag cagcacctcc agtggggcca gcacagccac 1050
caactctgac tccagcacag tgtccagtgg ggccagcact gccaccaact 1100
ctgagtccag cagcacctcc agtggggcca gcacagccac caactctgag 1150
tccagcacga cctccagtgg ggctagcaca gccaccaact ctgactccag 1200
cacaacctcc agtggggccg gcacagccac caactctgag tccagcacag 1250
tgtccagtgg gatcagcaca gtcaccaatt ctgagtccag cacacctcc 1300
agtggggcca acacagccac caactctgag tccagtacga cctccagtgg 1350
ggccaacaca gccaccaact ctgagtccag cacagtgtcc agtggggcca 1400
gactgccac caactctgag tccagcaca cctccagtgg ggtcagcaca 1450
gccaccaact ctgagtccag cacaacctcc agtggggcta gcacagccac 1500

Thr Asn Ser Glu Phe Ser Thr Ala Ser Ser Gly Ile Ser Ile Ala
 95 100 105

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 110 115 120

Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Ser Thr Val
 125 130 135

Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Ala Ser Thr Ala
 140 145 150

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
 155 160 165

Thr Asn Ser Glu Ser Ser Thr Leu Ser Ser Gly Ala Ser Thr Ala
 170 175 180

Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 185 190 195

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 200 205 210

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
 215 220 225

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 230 235 240

Thr Asn Ser Glu Ser Arg Thr Thr Ser Asn Gly Ala Gly Thr Ala
 245 250 255

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 260 265 270

Thr Asn Ser Asp Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala
 275 280 285

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 290 295 300

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 305 310 315

Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Gly Thr Ala
 320 325 330

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val
 335 340 345

Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Asn Thr Ala
 350 355 360

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala

	365	370	375
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Gly Ala Ser Thr	Ala
	380	385	390
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Val Ser Thr	Ala
	395	400	405
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala
	410	415	420
Thr Asn Ser Asp	Ser Ser Thr Thr Ser	Ser Glu Ala Ser Thr	Ala
	425	430	435
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Gly Ile Ser Thr	Val
	440	445	450
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Asn Thr	Ala
	455	460	465
Thr Asn Ser Gly	Ser Ser Val Thr Ser	Ala Gly Ser Gly Thr	Ala
	470	475	480
Ala Leu Thr Gly	Met His Thr Thr Ser	His Ser Ala Ser Thr	Ala
	485	490	495
Val Ser Glu Ala	Lys Pro Gly Gly Ser	Leu Val Pro Trp Glu	Ile
	500	505	510
Phe Leu Ile Thr	Leu Val Ser Val Val	Ala Ala Val Gly Leu	Phe
	515	520	525
Ala Gly Leu Phe	Phe Cys Val Arg Asn	Ser Leu Ser Leu Arg	Asn
	530	535	540
Thr Phe Asn Thr	Ala Val Tyr His Pro	His Gly Leu Asn His	Gly
	545	550	555
Leu Gly Pro Gly	Pro Gly Gly Asn His	Gly Ala Pro His Arg	Pro
	560	565	570
Arg Trp Ser Pro	Asn Trp Phe Trp Arg	Arg Pro Val Ser Ser	Ile
	575	580	585
Ala Met Glu Met	Ser Gly Arg Asn Ser	Gly Pro	
	590	595	

<210> 244
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

 <400> 244

gaagcaccag cctttatctc ttcacc 26
 <210> 245
 <211> 24
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic sequence.
 <400> 245
 gtcagagttg gtggctgtgc tagc 24
 <210> 246
 <211> 48
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial Sequence
 <222> 1-48
 <223> Synthetic construct.
 <400> 246
 ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48
 <210> 247
 <211> 957
 <212> DNA
 <213> Homo sapiens
 <400> 247
 gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcatcc 50
 ttcccgaacct tcccagcaat atgcatcttg cacgtctggt cggctcctgc 100
 tccctccttc tgctactggg gccctgtct ggatgggcgg ccagcgatga 150
 cccattgag aaggtcattg aagggatcaa ccgagggctg agcaatgcag 200
 agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250
 gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300
 ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350
 tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaaag 400
 gaagcagaga agcttggcca tgggggtcaac aacgctgctg gacaggccgg 450
 gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500
 ctgggaagga agcagagaaa cttggccaag ggggtcaacca tgctgctgac 550
 caggctggaa aggaagtgga gaagcttggc caaggtgccc accatgctgc 600

tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650
ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700
tccagccatc aaggaggggc cacaaccacg ccgttagcct ctggggcctc 750
agtcaacacg cctttcatca accttcccgc cctgtggagg agcgtcgcca 800
acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850
gttgtcacat cagctgacat gacctggagg ggttgggggt gggggacagg 900
tttctgaaat ccctgaaggg ggttgtactg ggatttgtga ataaacttga 950
tacacca 957

<210> 248
<211> 247
<212> PRT
<213> Homo sapiens

<400> 248
Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu Leu
1 5 10 15
Leu Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu
20 25 30
Lys Val Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg
35 40 45
Glu Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His
50 55 60
Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met
65 70 75
Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu
80 85 90
Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His Gly Ile
95 100 105
Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val Asn
110 115 120
Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln
125 130 135
Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys
140 145 150
Leu Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu
155 160 165
Val Glu Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala
170 175 180

Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser
 185 190 195

Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser
 200 205 210

Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly
 215 220 225

Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
 230 235 240

Ser Val Ala Asn Ile Met Pro
 245

<210> 249
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 249
 caatatgcat cttgcacgtc tgg 23

<210> 250
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 250
 aagcttctct gcttcctttc ctgc 24

<210> 251
 <211> 43
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-43
 <223> Synthetic construct.

<400> 251
 tgacccatt gagaaggta ttgaaggat caaccgaggg ctg 43

<210> 252
 <211> 3781
 <212> DNA
 <213> Homo sapiens

<400> 252

ctccgggtcc ccaggggctg cgccgggccc gcctggcaag ggggacgagt 50
cagtggacac tccaggaaga gcggccccgc ggggggcat gaccgtgcgc 100
tgacctgac tcaactcagg tccggaggcg ggggcccccg gggcgactcg 150
ggggcggaac gcggggcgga gctgcgcgcc gtgagtccgg ccgagccacc 200
tgagcccgag ccgcgggaca ccgtcgtccc tgctctccga atgctgcgca 250
ccgcgatggg cctgaggagc tggctcgcgc ccccatgggg cgcgctgcgc 300
cctcggccac cgctgctgct gctcctgctg ctgctgctcc tgctgcagcc 350
gccgcctccg acctgggcgc tcagcccccg gatcagcctg cctctgggct 400
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acagcccttc tgctgagcag ggatggcagg accctgtacg tgggtgctcg 500
agaggccctc tttgcaacta gtagcaacct cagcttcctg ccaggcgggg 550
agtaccagga gctgcttttg ggtgcagacg cagagaagaa acagcagtgc 600
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tcagcccat gtgtacctac atcaacatgg agaacttcac cctggcaagg 750
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agcggcctct acaaggaggt gaaccgtgag acacagcagt ggtacaccgt 1400
gacccacccg gtgcccacac ccgggcctgg agcgtgcac accaacagtg 1450

cccgggaaag gaagatcaac tcatccctgc agtcccaga ccgctgctg 1500
 aacttcctca aggaccactt cctgatggac gggcaggtcc gaagccgcat 1550
 gctgctgctg cagccccagg ctctctacca gcgctgggt gtacaccgctg 1600
 tccctggcct gcaccacacc tacgatgtcc tcttcctggg cactggtgac 1650
 ggccggctcc acaaggcagt gagcgtgggc ccccggtgc acatcattga 1700
 ggagctgcag atcttctcat cgggacagcc cgtgcagaat ctgctcctgg 1750
 acaccacag ggggctgctg tatgcggcct cacactcggg cgtagtccag 1800
 gtgcccattg ccaactgcag cctgtaccgg agctgtgggg actgcctcct 1850
 cggccgggac ccctactgtg cttggagcgg ctccagctgc aagcacgtca 1900
 gcctctacca gcctcagctg gccaccaggc cgtggatcca ggacatcgag 1950
 ggagccagcg ccaaggacct ttgcagcgcg tcttcggttg tgtccccgtc 2000
 ttttgtacca acaggggaga agccatgtga gcaagtccag ttccagccca 2050
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 ctctggctac gcaacggggc cccgtcaat gcctcggcct cctgccacgt 2150
 gctaccact ggggacctgc tgctggtggg cacccaacag ctgggggagt 2200
 tccagtgtg gtcactagag gagggcttcc agcagctggt agccagctac 2250
 tgccagagg tgggtggagga cggggtggca gaccaaacag atgaggggtg 2300
 cagtgtacc gtcattatca gcacatcgcg tgtgagtga ccagctggtg 2350
 gcaaggccag ctgggggtga gacaggtcct actggaagga gttcctggtg 2400
 atgtgcacgc tctttgtgct ggccgtgctg ctcccagttt tattcttgct 2450
 ctaccggcac cggaacagca tgaaagtctt cctgaagcag ggggaatgtg 2500
 ccagctgca cccaagacc tgccctgtgg tgctgcccc tgagaccgcg 2550
 ccactcaacg gcctagggcc ccctagcacc ccgctcgatc accgagggtg 2600
 ccagtccctg tcagacagcc cccggggg cgaagtctt actgagtcag 2650
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 gtgagagctg acttcagag gacgtgccc tggcttcagg ggctgtgaat 2800
 gctcggagag ggtcaactgg acctcccctc cgtctgtctc ttcgtggaac 2850
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ctctccagtc aagtagcgaa gctcctacca cccagacacc caaacagccg 2950
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 cagtgtcctt tatgtaaact gagccctttg tttaaaaaac aattccaaat 3050
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 ttgtctgaga cagagttgga aaccctcacc aactggcctc ttcaccttcc 3200
 acattatccc gctgccaccg gctgccctgt ctactgcag attcaggacc 3250
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 ggggcctca ccaggtcctg ggctcggacc caactcctgg acctttccag 3400
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 cctgccttcc tccgttggtg cgtgagaacc cgtgtgcccc ttcccaccat 3550
 atccaccctc gctccatctt tgaactcaaa cacgaggaac taactgcacc 3600
 ctggtcctct cccagtccc cagttcacc tccatccctc accttctctc 3650
 actctaaggg atatcaacac tgcccagcac aggggccctg aatttatgtg 3700
 gtttttatac attttttaat aagatgcact ttatgtcatt ttttaataaa 3750
 gtctgaagaa ttactgttta aaaaaaaaaa a 3781

<210> 253
 <211> 837
 <212> PRT
 <213> Homo sapiens

<400> 253
 Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp Leu Ala Ala Pro
 1 5 10 15
 Trp Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu
 20 25 30
 Leu Leu Leu Leu Leu Gln Pro Pro Pro Pro Thr Trp Ala Leu Ser
 35 40 45
 Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu
 50 55 60
 Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu
 65 70 75
 Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu

80								85						90	
Phe	Ala	Leu	Ser	Ser 95	Asn	Leu	Ser	Phe	Leu 100	Pro	Gly	Gly	Glu	Tyr 105	
Gln	Glu	Leu	Leu	Trp 110	Gly	Ala	Asp	Ala	Glu 115	Lys	Lys	Gln	Gln	Cys 120	
Ser	Phe	Lys	Gly	Lys 125	Asp	Pro	Gln	Arg	Asp 130	Cys	Gln	Asn	Tyr	Ile 135	
Lys	Ile	Leu	Leu	Pro 140	Leu	Ser	Gly	Ser	His 145	Leu	Phe	Thr	Cys	Gly 150	
Thr	Ala	Ala	Phe	Ser 155	Pro	Met	Cys	Thr	Tyr 160	Ile	Asn	Met	Glu	Asn 165	
Phe	Thr	Leu	Ala	Arg 170	Asp	Glu	Lys	Gly	Asn 175	Val	Leu	Leu	Glu	Asp 180	
Gly	Lys	Gly	Arg	Cys 185	Pro	Phe	Asp	Pro	Asn 190	Phe	Lys	Ser	Thr	Ala 195	
Leu	Val	Val	Asp	Gly 200	Glu	Leu	Tyr	Thr	Gly 205	Thr	Val	Ser	Ser	Phe 210	
Gln	Gly	Asn	Asp	Pro 215	Ala	Ile	Ser	Arg	Ser 220	Gln	Ser	Leu	Arg	Pro 225	
Thr	Lys	Thr	Glu	Ser 230	Ser	Leu	Asn	Trp	Leu 235	Gln	Asp	Pro	Ala	Phe 240	
Val	Ala	Ser	Ala	Tyr 245	Ile	Pro	Glu	Ser	Leu 250	Gly	Ser	Leu	Gln	Gly 255	
Asp	Asp	Asp	Lys	Ile 260	Tyr	Phe	Phe	Phe	Ser 265	Glu	Thr	Gly	Gln	Glu 270	
Phe	Glu	Phe	Phe	Glu 275	Asn	Thr	Ile	Val	Ser 280	Arg	Ile	Ala	Arg	Ile 285	
Cys	Lys	Gly	Asp	Glu 290	Gly	Gly	Glu	Arg	Val 295	Leu	Gln	Gln	Arg	Trp 300	
Thr	Ser	Phe	Leu	Lys 305	Ala	Gln	Leu	Leu	Cys 310	Ser	Arg	Pro	Asp	Asp 315	
Gly	Phe	Pro	Phe	Asn 320	Val	Leu	Gln	Asp	Val 325	Phe	Thr	Leu	Ser	Pro 330	
Ser	Pro	Gln	Asp	Trp 335	Arg	Asp	Thr	Leu	Phe 340	Tyr	Gly	Val	Phe	Thr 345	
Ser	Gln	Trp	His	Arg 350	Gly	Thr	Thr	Glu	Gly 355	Ser	Ala	Val	Cys	Val 360	
Phe	Thr	Met	Lys	Asp 365	Val	Gln	Arg	Val	Phe 370	Ser	Gly	Leu	Tyr	Lys 375	

Glu Val Asn Arg	Glu Thr Gln Gln Trp	Tyr Thr Val Thr His	Pro
380		385	390
Val Pro Thr Pro	Arg Pro Gly Ala Cys	Ile Thr Asn Ser Ala	Arg
395		400	405
Glu Arg Lys Ile	Asn Ser Ser Leu Gln	Leu Pro Asp Arg Val	Leu
410		415	420
Asn Phe Leu Lys	Asp His Phe Leu Met	Asp Gly Gln Val Arg	Ser
425		430	435
Arg Met Leu Leu	Leu Gln Pro Gln Ala	Arg Tyr Gln Arg Val	Ala
440		445	450
Val His Arg Val	Pro Gly Leu His His	Thr Tyr Asp Val Leu	Phe
455		460	465
Leu Gly Thr Gly	Asp Gly Arg Leu His	Lys Ala Val Ser Val	Gly
470		475	480
Pro Arg Val His	Ile Ile Glu Glu Leu	Gln Ile Phe Ser Ser	Gly
485		490	495
Gln Pro Val Gln	Asn Leu Leu Leu Asp	Thr His Arg Gly Leu	Leu
500		505	510
Tyr Ala Ala Ser	His Ser Gly Val Val	Gln Val Pro Met Ala	Asn
515		520	525
Cys Ser Leu Tyr	Arg Ser Cys Gly Asp	Cys Leu Leu Ala Arg	Asp
530		535	540
Pro Tyr Cys Ala	Trp Ser Gly Ser Ser	Cys Lys His Val Ser	Leu
545		550	555
Tyr Gln Pro Gln	Leu Ala Thr Arg Pro	Trp Ile Gln Asp Ile	Glu
560		565	570
Gly Ala Ser Ala	Lys Asp Leu Cys Ser	Ala Ser Ser Val Val	Ser
575		580	585
Pro Ser Phe Val	Pro Thr Gly Glu Lys	Pro Cys Glu Gln Val	Gln
590		595	600
Phe Gln Pro Asn	Thr Val Asn Thr Leu	Ala Cys Pro Leu Leu	Ser
605		610	615
Asn Leu Ala Thr	Arg Leu Trp Leu Arg	Asn Gly Ala Pro Val	Asn
620		625	630
Ala Ser Ala Ser	Cys His Val Leu Pro	Thr Gly Asp Leu Leu	Leu
635		640	645
Val Gly Thr Gln	Gln Leu Gly Glu Phe	Gln Cys Trp Ser Leu	Glu
650		655	660
Glu Gly Phe Gln	Gln Leu Val Ala Ser	Tyr Cys Pro Glu Val	Val

<400> 255
tgaagccagg gcagcgtcct ctgg 24

<210> 256
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 256
gtacaggctg cagttggc 18

<210> 257
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 257
agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 258
gagctgcaga tcttctcatc gggacagccc gtgcagaatc tgctc 45

<210> 259
<211> 4563
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 3635
<223> unknown base

<400> 259
ctaagccgga ggatgtgcag ctgcggcggc ggcgccggct acgaagagga 50
cggggacagg cgccgtgcga accgagccca gccagccgga ggacgcgggc 100
agggcgggac gggagcccgg actcgtctgc cgccgccgtc gtcgccgtcg 150

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<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

Met Ala Ala Arg Gly Arg Arg Ala Trp Leu Ser Val Leu Leu Gly
1 5 10 15

Leu Val Leu Gly Phe Val Leu Ala Ser Arg Leu Val Leu Pro Arg
20 25 30

Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro
35 40 45

Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly
50 55 60

Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser
65 70 75

Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly
80 85 90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala
95 100 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe
110 115 120

Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro
125 130 135

Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
140 145 150

Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu
155 160 165

Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg
170 175 180

Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe
185 190 195

Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu
200 205 210

Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val
215 220 225

Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
230 235 240

Lys Cys Leu Arg	Glu Met Tyr Thr Thr	His Glu Asp Val Glu Val	245	250	255
Gly Arg Cys Val	Arg Arg Phe Ala Gly	Val Gln Cys Val Trp Ser	260	265	270
Tyr Glu Met Arg	Gln Leu Phe Tyr Glu	Asn Tyr Glu Gln Asn Lys	275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn	Ser Lys Ile His Gln Ala	290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro	Pro Tyr Gln Tyr Arg Leu	305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile	Ser Glu Leu Arg His Arg	320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val	Leu Met Ser Lys Tyr Ser	335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu	Gln Leu Gly Ile Pro Pro	350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln	Arg Glu Glu Ile Leu Glu	365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu	Tyr Ser Ala Val Asp Gly	380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser	Ala Gln Arg Glu Ala Leu	395	400	405
Asp Asp Ile Val	Met Gln Val Met Glu	Met Ile Asn Ala Asn Ala	410	415	420
Lys Thr Arg Gly	Arg Ile Ile Asp Phe	Lys Glu Ile Gln Tyr Gly	425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly	Ala Glu Tyr Ile Leu Asp	440	445	450
Leu Leu Leu Leu	Tyr Lys Lys His Lys	Gly Lys Lys Met Thr Val	455	460	465
Pro Val Arg Arg	His Ala Tyr Leu Gln	Gln Thr Phe Ser Lys Ile	470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp	Ala Gln Glu Leu Ala Lys	485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu	Ser Phe Leu Ser Asn Ser	500	505	510
Leu Lys Lys Leu	Val Pro Phe Gln Leu	Pro Gly Ser Lys Ser Glu	515	520	525
His Lys Glu Pro	Lys Asp Lys Lys Ile	Asn Ile Leu Ile Pro Leu			

530					535					540				
Ser	Gly	Arg	Phe	Asp	Met	Phe	Val	Arg	Phe	Met	Gly	Asn	Phe	Glu
				545					550					555
Lys	Thr	Cys	Leu	Ile	Pro	Asn	Gln	Asn	Val	Lys	Leu	Val	Val	Leu
				560					565					570
Leu	Phe	Asn	Ser	Asp	Ser	Asn	Pro	Asp	Lys	Ala	Lys	Gln	Val	Glu
				575					580					585
Leu	Met	Arg	Asp	Tyr	Arg	Ile	Lys	Tyr	Pro	Lys	Ala	Asp	Met	Gln
				590					595					600
Ile	Leu	Pro	Val	Ser	Gly	Glu	Phe	Ser	Arg	Ala	Leu	Ala	Leu	Glu
				605					610					615
Val	Gly	Ser	Ser	Gln	Phe	Asn	Asn	Glu	Ser	Leu	Leu	Phe	Phe	Cys
				620					625					630
Asp	Val	Asp	Leu	Val	Phe	Thr	Thr	Glu	Phe	Leu	Gln	Arg	Cys	Arg
				635					640					645
Ala	Asn	Thr	Val	Leu	Gly	Gln	Gln	Ile	Tyr	Phe	Pro	Ile	Ile	Phe
				650					655					660
Ser	Gln	Tyr	Asp	Pro	Lys	Ile	Val	Tyr	Ser	Gly	Lys	Val	Pro	Ser
				665					670					675
Asp	Asn	His	Phe	Ala	Phe	Thr	Gln	Lys	Thr	Gly	Phe	Trp	Arg	Asn
				680					685					690
Tyr	Gly	Phe	Gly	Ile	Thr	Cys	Ile	Tyr	Lys	Gly	Asp	Leu	Val	Arg
				695					700					705
Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln	Gly	Trp	Gly	Leu	Glu	Asp
				710					715					720
Val	Asp	Leu	Phe	Asn	Lys	Val	Val	Gln	Ala	Gly	Leu	Lys	Thr	Phe
				725					730					735
Arg	Ser	Gln	Glu	Val	Gly	Val	Val	His	Val	His	His	Pro	Val	Phe
				740					745					750
Cys	Asp	Pro	Asn	Leu	Asp	Pro	Lys	Gln	Tyr	Lys	Met	Cys	Leu	Gly
				755					760					765
Ser	Lys	Ala	Ser	Thr	Tyr	Gly	Ser	Thr	Gln	Gln	Leu	Ala	Glu	Met
				770					775					780
Trp	Leu	Glu	Lys	Asn	Asp	Pro	Ser	Tyr	Ser	Lys	Ser	Ser	Asn	Asn
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Asn	Gly	Ser	Val	Arg	Thr	Ala								
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<210> 261
<211> 24

<212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 261
 gtgccactac ggggtgtgga cgac 24

<210> 262
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 262
 tcccatttct tccgtggtgc ccag 24

<210> 263
 <211> 46
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-46
 <223> Synthetic construct.

<400> 263
 ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264
 <211> 1419
 <212> DNA
 <213> Homo sapiens

<400> 264
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 tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200
 agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250
 agtttttagag aacctagtag gaagtgttcc ctctggggag ccaggtcgtg 300
 agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350
 tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

tgttttaacc aatcctatca gtgaagaaac tacaactttc cctacaggag 450
 gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccgccattc 500
 tgggtcgatca aaccaaacaa tgtttccatt gttttgcatg cagaggaacc 550
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<210> 265
 <211> 350
 <212> PRT
 <213> Homo sapiens

<400> 265
 Met Lys Pro Leu Val Leu Leu Val Ala Leu Leu Leu Trp Pro Ser
 1 5 10 15
 Ser Val Pro Ala Tyr Pro Ser Ile Thr Val Thr Pro Asp Glu Glu
 20 25 30
 Gln Asn Leu Asn His Tyr Ile Gln Val Leu Glu Asn Leu Val Arg
 35 40 45
 Ser Val Pro Ser Gly Glu Pro Gly Arg Glu Lys Lys Ser Asn Ser

50					55					60				
Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys
				65					70					75
Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu
				80					85					90
Thr	Asn	Pro	Ile	Ser	Glu	Glu	Thr	Thr	Thr	Phe	Pro	Thr	Gly	Gly
				95					100					105
Phe	Thr	Pro	Glu	Ile	Gly	Lys	Lys	Lys	His	Thr	Glu	Ser	Thr	Pro
				110					115					120
Phe	Trp	Ser	Ile	Lys	Pro	Asn	Asn	Val	Ser	Ile	Val	Leu	His	Ala
				125					130					135
Glu	Glu	Pro	Tyr	Ile	Glu	Asn	Glu	Glu	Pro	Glu	Pro	Glu	Pro	Glu
				140					145					150
Pro	Ala	Ala	Lys	Gln	Thr	Glu	Ala	Pro	Arg	Met	Leu	Pro	Val	Val
				155					160					165
Thr	Glu	Ser	Ser	Thr	Ser	Pro	Tyr	Val	Thr	Ser	Tyr	Lys	Ser	Pro
				170					175					180
Val	Thr	Thr	Leu	Asp	Lys	Ser	Thr	Gly	Ile	Glu	Ile	Ser	Thr	Glu
				185					190					195
Ser	Glu	Asp	Val	Pro	Gln	Leu	Ser	Gly	Glu	Thr	Ala	Ile	Glu	Lys
				200					205					210
Pro	Glu	Glu	Phe	Gly	Lys	His	Pro	Glu	Ser	Trp	Asn	Asn	Asp	Asp
				215					220					225
Ile	Leu	Lys	Lys	Ile	Leu	Asp	Ile	Asn	Ser	Gln	Val	Gln	Gln	Ala
				230					235					240
Leu	Leu	Ser	Asp	Thr	Ser	Asn	Pro	Ala	Tyr	Arg	Glu	Asp	Ile	Glu
				245					250					255
Ala	Ser	Lys	Asp	His	Leu	Lys	Arg	Ser	Leu	Ala	Leu	Ala	Ala	Ala
				260					265					270
Ala	Glu	His	Lys	Leu	Lys	Thr	Met	Tyr	Lys	Ser	Gln	Leu	Leu	Pro
				275					280					285
Val	Gly	Arg	Thr	Ser	Asn	Lys	Ile	Asp	Asp	Ile	Glu	Thr	Val	Ile
				290					295					300
Asn	Met	Leu	Cys	Asn	Ser	Arg	Ser	Lys	Leu	Tyr	Glu	Tyr	Leu	Asp
				305					310					315
Ile	Lys	Cys	Val	Pro	Pro	Glu	Met	Arg	Glu	Lys	Ala	Ala	Thr	Val
				320					325					330
Phe	Asn	Thr	Leu	Lys	Asn	Met	Cys	Arg	Ser	Arg	Arg	Val	Thr	Ala
				335					340					345

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aaa 2403

<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

Met	Ala	Phe	Val	Leu	Ile	Leu	Val	Leu	Ser	Phe	Tyr	Glu	Leu	Val
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Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

20					25					30				
Leu	Val	Gly	Glu	Asp	Ala	Val	Phe	Ser	Cys	Ser	Leu	Phe	Pro	Glu
				35					40					45
Thr	Ser	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Asn	Gln	Phe
				50					55					60
His	Ala	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Glu	Asp	Trp	Glu	Ser
				65					70					75
Lys	Gln	Met	Pro	Gln	Tyr	Arg	Gly	Arg	Thr	Glu	Phe	Val	Lys	Asp
				80					85					90
Ser	Ile	Ala	Gly	Gly	Arg	Val	Ser	Leu	Arg	Leu	Lys	Asn	Ile	Thr
				95					100					105
Pro	Ser	Asp	Ile	Gly	Leu	Tyr	Gly	Cys	Trp	Phe	Ser	Ser	Gln	Ile
				110					115					120
Tyr	Asp	Glu	Glu	Ala	Thr	Trp	Glu	Leu	Arg	Val	Ala	Ala	Leu	Gly
				125					130					135
Ser	Leu	Pro	Leu	Ile	Ser	Ile	Val	Gly	Tyr	Val	Asp	Gly	Gly	Ile
				140					145					150
Gln	Leu	Leu	Cys	Leu	Ser	Ser	Gly	Trp	Phe	Pro	Gln	Pro	Thr	Ala
				155					160					165
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Ser	Asp	Ser	Arg
				170					175					180
Ala	Asn	Ala	Asp	Gly	Tyr	Ser	Leu	Tyr	Asp	Val	Glu	Ile	Ser	Ile
				185					190					195
Ile	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Leu	Cys	Ser	Ile	His	Leu
				200					205					210
Ala	Glu	Gln	Ser	His	Glu	Val	Glu	Ser	Lys	Val	Leu	Ile	Gly	Glu
				215					220					225
Thr	Phe	Phe	Gln	Pro	Ser	Pro	Trp	Arg	Leu	Ala	Ser	Ile	Leu	Leu
				230					235					240
Gly	Leu	Leu	Cys	Gly	Ala	Leu	Cys	Gly	Val	Val	Met	Gly	Met	Ile
				245					250					255
Ile	Val	Phe	Phe	Lys	Ser	Lys	Gly	Lys	Ile	Gln	Ala	Glu	Leu	Asp
				260					265					270
Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys
				275					280					285
His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys
				290					295					300
Leu	Cys	Val	Ser	Asp	Leu	Lys	Thr	Val	Thr	His	Arg	Lys	Ala	Pro
				305					310					315

Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val
320 325 330
Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val
335 340 345
Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp
350 355 360
Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn
365 370 375
Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr
380 385 390
Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr
395 400 405
Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe
410 415 420
Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys
425 430 435
Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr
440 445 450
Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp
455 460 465

Gly

<210> 268
<211> 2103
<212> DNA
<213> Homo sapiens

<400> 268
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gtcatcttca tatccctgat tgtcctggca gtgtgcattg gactcactgt 150
tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250
aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300
attttataaa tctccattaa ggaagaatt tgtcaagtct caggttatca 350
agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400
agatttcact ctactgagga tcttgaaact gtagataaaa ttgttcaact 450
tgttttacat gaaaagctgc aagatgctgt aggaccccct aaagtagatc 500

ctcactcagt taaaattaaa aaaatcaaca agacagaaac agacagctat 550
ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600
caggatcgtt ggtgggacag aagtagaaga gggatgaatgg ccctggcagg 650
ctagcctgca gtgggatggg agtcatcgct gtggagcaac cttaattaat 700
gccacatggc ttgtgagtgc tgctcactgt ttacaacat ataagaaccc 750
tgccagatgg actgcttctt ttggagtaac aataaacct tcgaaaatga 800
aacggggtct ccggagaata attgtccatg aaaaatacaa acacccatca 850
catgactatg atatttctct tgcagagctt tctagccctg ttccctacac 900
aatgacgta catagagttt gtctccctga tgcctcctat gagtttcaac 950
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tacagtcaaa atcatcttcg acaagcacag gtgactctca tagacgctac 1050
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tatgtgctgg ctcccttagaa ggaaaaacag atgcatgcca gggatgactct 1150
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cagaattttg acttggtgac ataaatttgt aatgcatata tacaatttga 1650
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tcccctacat ttatttggca cagaaaagta ttaggtgttt ttcttagtgg 1800
aatattagaa atgatcatat tcattatgaa aggtcaagca aagacagcag 1850
aataccaatc acttcatcat ttaggaagta tgggaactaa gttaaggaag 1900
tccagaaaga agccaagata tacccttatt ttcatttcca aacaactact 1950

<210> 269
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 269
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 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr
 35 40 45
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
 50 55 60
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
 65 70 75
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
 80 85 90
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
 95 100 105
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
 110 115 120
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
 125 130 135
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
 140 145 150
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
 155 160 165
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
 170 175 180
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
 185 190 195
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
 200 205 210
 Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
 215 220 225

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ggccggcggc ctgcctgtgc ccaggactct ccagccccgc ccagccgccc 400
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ttaaaaaaaaa aaaaaaaaaa 1170

<210> 271
<211> 238
<212> PRT
<213> Homo sapiens

<400> 271
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Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala
35 40 45
Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys
50 55 60
Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly
65 70 75

Leu Ser Ser Pro Ala Gln Pro Pro Asp Pro Pro Arg Met Gly Glu
80 85 90

Val Arg Ile Ala Ala Glu Glu Gly Arg Ala Val Val His Trp Cys
95 100 105

Ala Pro Phe Ser Pro Val Leu His Tyr Trp Leu Leu Leu Trp Asp
110 115 120

Gly Ser Glu Ala Ala Gln Lys Gly Pro Pro Leu Asn Ala Thr Val
125 130 135

Arg Arg Ala Glu Leu Lys Gly Leu Lys Pro Gly Gly Ile Tyr Val
140 145 150

Val Cys Val Val Ala Ala Asn Glu Ala Gly Ala Ser Arg Val Pro
155 160 165

Gln Ala Gly Gly Glu Gly Leu Glu Gly Ala Asp Ile Pro Ala Phe
170 175 180

Gly Pro Cys Ser Arg Leu Ala Val Pro Pro Asn Pro Arg Thr Leu
185 190 195

Val His Ala Ala Val Gly Val Gly Thr Ala Leu Ala Leu Leu Ser
200 205 210

Cys Ala Ala Leu Val Trp His Phe Cys Leu Arg Asp Arg Trp Gly
215 220 225

Cys Pro Arg Arg Ala Ala Ala Arg Ala Ala Gly Ala Leu
230 235

<210> 272
<211> 2397
<212> DNA
<213> Homo sapiens

<400> 272
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cccaggcggg cgtggggcac cgggccccagc gccgacgac gctgccgttt 150
tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200
gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgcctgctct 250
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aacgagggta gaggaagcag tcattttgac ttactttcct gtggttcac 400
cggatcatgat tgctgtttgc tgtttcotta tcattgtggg gatgttagga 450
tattgtggaa cggtgaaaag aaatctgttg cttcttgcat ggtactttgg 500

aagtttgctt gtcattttct gtgtagaact ggcttgtggc gtttggacat 550
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aaagccagga tgacaaaatta tggattacct agatatcggt ggcttactca 650
tgcttggaat ttttttcaga gagagttaa gtgctgtgga gtagtatatt 700
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tgtgttagag aattcccagg atgttccaaa caggcccacc aggaagatct 800
cagtgcactt tatcaagagg gttgtgggaa gaaaatgtat tcctttttga 850
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gtgacacaaa tcctggccat gattctcacc attactctgc tctgggctct 950
gtattatgat agaagggagc ctgggacaga ccaaattgat tccttgaaga 1000
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agcctgtcaa gaatctttga acacacatcc atggcaaaca gctttaatac 1100
acactttgag atggaggagt tataaaaaga aatgtcacag aagaaaacca 1150
caaaactgtt ttattggact tgtgaatttt tgagtacata ctatgtgttt 1200
cagaaatatg tagaaataaa aatgttgcca taaaataaca cctaagcata 1250
tactattcta tgctttaaaa tgaggatgga aaagtttcat gtcataagtc 1300
accacctgga caataattga tgcccttaaa atgctgaaga cagatgtcat 1350
accactgtg tagcctgtgt atgactttta ctgaacacag ttatgttttg 1400
aggcagcatg gtttgattag catttccgca tccatgcaaa cgagtcacat 1450
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cagaaaactt tcaatattgg tgactacct aatgtgattt ttgctgggta 1650
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ttgtcctgta tagcatcatt attttttagcc tttcctgtta ataaagcttt 1850
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taaccactaa ttttgaaaat taccagtgtg atacatagga atcattattc 1950

	170		175		180
Cys Cys Val Arg	Glu Phe Pro Gly Cys	Ser Lys Gln Ala His	Gln		
	185		190		195
Glu Asp Leu Ser	Asp Leu Tyr Gln Glu	Gly Cys Gly Lys Lys	Met		
	200		205		210
Tyr Ser Phe Leu	Arg Gly Thr Lys Gln	Leu Gln Val Leu Arg	Phe		
	215		220		225
Leu Gly Ile Ser	Ile Gly Val Thr Gln	Ile Leu Ala Met Ile	Leu		
	230		235		240
Thr Ile Thr Leu	Leu Trp Ala Leu Tyr	Tyr Asp Arg Arg Glu	Pro		
	245		250		255
Gly Thr Asp Gln	Met Met Ser Leu Lys	Asn Asp Asn Ser Gln	His		
	260		265		270
Leu Ser Cys Pro	Ser Val Glu Leu Leu	Lys Pro Ser Leu Ser	Arg		
	275		280		285
Ile Phe Glu His	Thr Ser Met Ala Asn	Ser Phe Asn Thr His	Phe		
	290		295		300
Glu Met Glu Glu	Leu				
	305				

<210> 274
 <211> 2063
 <212> DNA
 <213> Homo sapiens

<400> 274
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 ttctgacctg ctggccagcc aggacctgtg tggggaggcc ctctgtctgc 150
 cttgggggtga caatctcagc tccaggctac agggagaccg ggaggatcac 200
 agagccagca tgttacagga tcctgacagt gatcaacctc tgaacagcct 250
 cgatgtcaaa ccctgcgca aaccccgat ccccatggag accttcagaa 300
 aggtggggat ccccatcatc atagcactac tgagcctggc gagtatcatc 350
 attgtggttg tcctcatcaa ggtgattctg gataaatact acttcctctg 400
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 tggactgtcc cttgggggag gacgaggagc actgtgtcaa gagcttcccc 500
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aaacagccag gagcttcgca tgcggaactc aagtggggccc tgtctctcag 750
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ttgggtacac ccctctgccc acagcctcag catttcttgg agcagcaaag 1650
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tactgtggg ctggagagga gaaggaaagg gtctgcgcca gccctgtccg 1900
tcttcacca tcccaagcc tactagagca agaaaccagt tgtaataata 1950
aatgcactgc cctactgttg gtatgactac cgttacctac tgttgctatt 2000
gttattacag ctatggccac tattattaaa gagctgtgta acatctctgg 2050

caaaaaaaaaaaa aaa 2063

<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp
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Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg
20 25 30

Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser
35 40 45

Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr
50 55 60

Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
65 70 75

Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu
80 85 90

His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg
95 100 105

Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr
110 115 120

Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu
125 130 135

Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu
140 145 150

Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn
155 160 165

Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser
170 175 180

Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu
185 190 195

Lys Thr Pro Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser
200 205 210

Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys
215 220 225

Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His
230 235 240

Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala
245 250 255

Gly	Ser	Asp	Lys	Leu	Gly	Ser	Phe	Pro	Ser	Leu	Ala	Val	Ala	Lys
				260					265					270
Ile	Ile	Ile	Ile	Glu	Phe	Asn	Pro	Met	Tyr	Pro	Lys	Asp	Asn	Asp
				275					280					285
Ile	Ala	Leu	Met	Lys	Leu	Gln	Phe	Pro	Leu	Thr	Phe	Ser	Gly	Thr
				290					295					300
Val	Arg	Pro	Ile	Cys	Leu	Pro	Phe	Phe	Asp	Glu	Glu	Leu	Thr	Pro
				305					310					315
Ala	Thr	Pro	Leu	Trp	Ile	Ile	Gly	Trp	Gly	Phe	Thr	Lys	Gln	Asn
				320					325					330
Gly	Gly	Lys	Met	Ser	Asp	Ile	Leu	Leu	Gln	Ala	Ser	Val	Gln	Val
				335					340					345
Ile	Asp	Ser	Thr	Arg	Cys	Asn	Ala	Asp	Asp	Ala	Tyr	Gln	Gly	Glu
				350					355					360
Val	Thr	Glu	Lys	Met	Met	Cys	Ala	Gly	Ile	Pro	Glu	Gly	Gly	Val
				365					370					375
Asp	Thr	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Tyr	Gln	Ser
				380					385					390
Asp	Gln	Trp	His	Val	Val	Gly	Ile	Val	Ser	Trp	Gly	Tyr	Gly	Cys
				395					400					405
Gly	Gly	Pro	Ser	Thr	Pro	Gly	Val	Tyr	Thr	Lys	Val	Ser	Ala	Tyr
				410					415					420
Leu	Asn	Trp	Ile	Tyr	Asn	Val	Trp	Lys	Ala	Glu	Leu			
				425					430					

<210> 276
 <211> 3143
 <212> DNA
 <213> Homo sapiens

<400> 276
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 ttttcctctt ccaactgctt cagctgctgc tgccgacgac gaccgcgggg 200
 ggaggcgggc aggggcccac gccaggggtc agatactatg caggggatga 250
 acgtagggca cttagcttct tccaccagaa gggcctccag gatcttgaca 300
 ctctgctcct gagggtgat ggaaatactc tctacgtggg ggctcgagaa 350
 gccattctgg ccttgatat ccaggatcca ggggtcccca ggctaaagaa 400

catgataccg tggccagcca gtgacagaaa aaagagtga tgtgccttta 450
 agaagaagag caatgagaca cagtgtttca acttcatccg tgtcctggtt 500
 tcttacaatg tcacccatct ctacacctgc ggcaccttcg ccttcagccc 550
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 aagcatacgg ctgtcttggg ggatgggatg ctctattctg gtactatgaa 700
 caacttctcg ggcagtgagc ccatcctgat gcgcacactg ggatcccagc 750
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 gcccttcaac gtcacccgc acgcggctc gctccccgc gattctccca 1050
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 accaggagct ctgcggtttg tgccttctct ctcttgaca ttgaacgtgt 1150
 ctttaagggg aaatacaaag agttgaaca agaaacttca cgctggacta 1200
 cttatagggg ccctgagacc aacccccgc caggcagttg ctacgtgggc 1250
 cctcctctg ataaggcct gacctcatg aaggaccatt tcctgatgga 1300
 tgagcaagtg gtggggacgc cctgctggt gaaatctggc gtggagtata 1350
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 ctatgagagc tgtgtggact gtgtccttgc ccgggacccc cactgtgcct 1650
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<210> 277
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 <213> Homo sapiens
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Gly Gly Thr Arg	Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu Asp
335	340	345
Ile Glu Arg Val	Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys Glu
350	355	360
Thr Ser Arg Trp	Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro Arg
365	370	375
Pro Gly Ser Cys	Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu Thr
380	385	390
Phe Met Lys Asp	His Phe Leu Met Asp	Glu Gln Val Val Gly Thr
395	400	405
Pro Leu Leu Val	Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala Val
410	415	420
Glu Thr Ala Gln	Gly Leu Asp Gly His	Ser His Leu Val Met Tyr
425	430	435
Leu Gly Thr Thr	Thr Gly Ser Leu His	Lys Ala Val Val Ser Gly
440	445	450
Asp Ser Ser Ala	His Leu Val Glu Glu	Ile Gln Leu Phe Pro Asp
455	460	465
Pro Glu Pro Val	Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly Ala
470	475	480
Val Phe Val Gly	Phe Ser Gly Gly Val	Trp Arg Val Pro Arg Ala
485	490	495
Asn Cys Ser Val	Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala Arg
500	505	510
Asp Pro His Cys	Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys Leu
515	520	525
Leu Ser Ala Pro	Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu Arg
530	535	540
Gly Asn Pro Glu	Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg Ser
545	550	555
Leu Arg Pro Gln	Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu Ala
560	565	570
Val Pro Asn Ser	Ile Leu Glu Leu Pro	Cys Pro His Leu Ser Ala
575	580	585

Leu Ala Ser Tyr Tyr Trp Ser His Gly Pro Ala Ala Val Pro Glu
590 595 600

Ala Ser Ser Thr Val Tyr Asn Gly Ser Leu Leu Leu Ile Val Gln
605 610 615

Asp Gly Val Gly Gly Leu Tyr Gln Cys Trp Ala Thr Glu Asn Gly
620 625 630

Phe Ser Tyr Pro Val Ile Ser Tyr Trp Val Asp Ser Gln Asp Gln
635 640 645

Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly Ile Pro Arg Glu His
650 655 660

Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly Ala Ala Leu Ala
665 670 675

Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val Thr Val Leu
680 685 690

Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val Ala Ser
695 700 705

Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys Glu
710 715 720

Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His
725 730 735

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740 745 750

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<210> 278
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 278
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<210> 279
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<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

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<400> 279
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<210> 280
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<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 280
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<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
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Leu	Met	Glu	Lys	Pro	Ile	Lys	Pro	Val	Pro	Gln	Asp	Leu	Glu	Asn
				275					280					285
Phe	Ile	Ala	Lys	Phe	Gly	Asp	Ser	Gly	Phe	Val	Leu	Val	Thr	Leu
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Gly	Ser	Met	Val	Asn	Thr	Cys	Gln	Asn	Pro	Glu	Ile	Phe	Lys	Glu
				305					310					315
Met	Asn	Asn	Ala	Phe	Ala	His	Leu	Pro	Gln	Gly	Val	Ile	Trp	Lys
				320					325					330
Cys	Gln	Cys	Ser	His	Trp	Pro	Lys	Asp	Val	His	Leu	Ala	Ala	Asn
				335					340					345
Val	Lys	Ile	Val	Asp	Trp	Leu	Pro	Gln	Ser	Asp	Leu	Leu	Ala	His
				350					355					360
Pro	Ser	Ile	Arg	Leu	Phe	Val	Thr	His	Gly	Gly	Gln	Asn	Ser	Ile
				365					370					375
Met	Glu	Ala	Ile	Gln	His	Gly	Val	Pro	Met	Val	Gly	Ile	Pro	Leu
				380					385					390
Phe	Gly	Asp	Gln	Pro	Glu	Asn	Met	Val	Arg	Val	Glu	Ala	Lys	Lys
				395					400					405
Phe	Gly	Val	Ser	Ile	Gln	Leu	Lys	Lys	Leu	Lys	Ala	Glu	Thr	Leu
				410					415					420
Ala	Leu	Lys	Met	Lys	Gln	Ile	Met	Glu	Asp	Lys	Arg	Tyr	Lys	Ser
				425					430					435
Ala	Ala	Val	Ala	Ala	Ser	Val	Ile	Leu	Arg	Ser	His	Pro	Leu	Ser
				440					445					450
Pro	Thr	Gln	Arg	Leu	Val	Gly	Trp	Ile	Asp	His	Val	Leu	Gln	Thr
				455					460					465
Gly	Gly	Ala	Thr	His	Leu	Lys	Pro	Tyr	Val	Phe	Gln	Gln	Pro	Trp
				470					475					480
His	Glu	Gln	Tyr	Leu	Phe	Asp	Val	Phe	Val	Phe	Leu	Leu	Gly	Leu
				485					490					495
Thr	Leu	Gly	Thr	Leu	Trp	Leu	Cys	Gly	Lys	Leu	Leu	Gly	Met	Ala
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 <212> DNA
 <213> Artificial

<220>
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 <222> 1-24
 <223> Synthetic construct.

<400> 283
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<210> 284
 <211> 24
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<220>
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 <222> 1-24
 <223> Synthetic construct.

<400> 284
 tcaggctggt ctccaaagag aggg 24

<210> 285
 <211> 45
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-45
 <223> Synthetic construct.

<400> 285
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<210> 286
 <211> 2340
 <212> DNA
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<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

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Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80					85					90
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
				95					100					105
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
				110					115					120
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
				125					130					135
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
				140					145					150
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
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Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser

<210>	288
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<222> 1-24
<223> Synthetic construct.

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<211> 27
<212> DNA
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<220>
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<222> 1-27
<223> Synthetic construct.

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<212> DNA
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<220>
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<222> 1-42
<223> Synthetic construct.

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<212> DNA
<213> Homo sapiens
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279

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<400> 292

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				20					25					30
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser
				35					40					45
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn
				50					55					60
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln
				65					70					75
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile
				80					85					90
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu
				95					100					105
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly
				110					115					120
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr
				125					130					135
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu
				140					145					150
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile
				155					160					165
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu
				170					175					180
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu
				185					190					195
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser
				200					205					210
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu
				215					220					225
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly
				230					235					240
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr
				245					250					255
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly

Ala Asp Leu Val	Pro Ile Tyr Ser Phe	Gly Glu Asn Glu Val Tyr
275	280	285
Lys Gln Val Ile	Phe Glu Glu Gly Ser Trp	Gly Arg Trp Val Gln
290	295	300
Lys Lys Phe Gln	Lys Tyr Ile Gly Phe	Ala Pro Cys Ile Phe His
305	310	315
Gly Arg Gly Leu	Phe Ser Ser Asp Thr	Trp Gly Leu Val Pro Tyr
320	325	330
Ser Lys Pro Ile	Thr Thr Val Val Gly	Glu Pro Ile Thr Ile Pro
335	340	345
Lys Leu Glu His	Pro Thr Gln Gln Asp	Ile Asp Leu Tyr His Thr
350	355	360
Met Tyr Met Glu	Ala Leu Val Lys Leu	Phe Asp Lys His Lys Thr
365	370	375
Lys Phe Gly Leu	Pro Glu Thr Glu Val	Leu Glu Val Asn
380	385	

<210> 293
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 293
 gctgacctgg ttcccatcta ctcc 24

<210> 294
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 294
 cccacagaca cccatgacac ttcc 24

<210> 295
 <211> 50
 <212> DNA
 <213> Artificial

<220>

<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 295
aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296
<211> 3060
<212> DNA
<213> Homo sapiens

<400> 296
gggcggcggg atggggggccg ggggcggcgg gcgccgcact cgctgaggcc 50
ccgacgcagg gccggggccg gccccaggcc gaggagcgcg gcggccagag 100
cggggcccgc gaggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200
ggctctgctg accttgtgcc ttggacggct gtcctcagcg aggggccgtg 250
caccgctcc tgagcagcgc catgggcctg ctggccttcc tgaagacca 300
gttcgtgctg cacctgctgg tcggctttgt cttcgtggcg agtggctctg 350
tcatcaactt cgtccagctg tgcacgctgg cgctctggcc ggtcagcaag 400
cagctctacc gcgcctcaa ctgccgcctc gcctactcac tctggagcca 450
actggctcatg ctgctggagt ggtggctctg cacggagtgt aactgttca 500
cggaccaggc cagggtagag cgctttggga aggagcacgc agtcatcatc 550
ctcaaccaca acttcgagat cgacttctc tgtgggtgga ccatgtgtga 600
gcgcttcgga gtgctggga gctccaagg cctcgctaag aaggagctgc 650
tctacgtgcc cctcatcggc tggacgtgg actttctgga gattgtgttc 700
tgcaagcggg agtgggagga ggaccgggac accgtggtcg aagggtgag 750
gcgcctgtcg gactaccccg agtacatgtg gtttctcctg tactgagag 800
ggacgcgctt cacggagacc aagcaccgcg ttagcatgga ggtggcggct 850
gctaaggggc ttcctgtcct caagtaccac ctgctgccgc ggaccaaggg 900
cttcaccacc gcagtcaagt gcctccgggg gacagtcgca gctgtctatg 950
atgtaaccct gaacttcaga ggaaacaaga acccgctccct gctggggatc 1000
ctctacggga agaagtacga ggcggacatg tgctgagga gatttctct 1050
ggaagacatc ccgctggatg aaaaggaagc agctcagtgg cttcataaac 1100
tgtaccagga gaaggacgcg ctccaggaga tatataatca gaaggcatg 1150

tttccagggg agcagtttaa gcctgcccg aggccgtgga ccctcctgaa 1200
 cttcctgtcc tgggccacca ttctcctgtc tcccctcttc agttttgtct 1250
 tgggcgtctt tgccagcggg tcacctctcc tgatcctgac tttcttgagg 1300
 tttgtgggag cagcttcctt tggagttcgc agactgatag gagaatcgct 1350
 tgaacctggg aggtggagat tgcagtgagc tgagatggca tcaactgtact 1400
 ccagcctagg caacagagca agactcagtc tcaaaaaaaaa aaaaaaacia 1450
 aaaaacccca gaaattcttg agttgaactg tgtagttact gacatgaaaa 1500
 attcactaga ggctgaacag cagatttgag caggcagaaa aaaatcagca 1550
 agcttgaaga tggtaacctg agatTTTTca ggctaataaa aaaagaatga 1600
 agaaaaatta acagcctcag agaccatgg tgcaccgtca cacaatacaa 1650
 catatgcatg atgagagtcc cagaaggaga ggagagaaag ggtcagaaag 1700
 aatggccaca agctgatgaa aaacagtaac ctaccactc aggaagctca 1750
 gtgaactcca atgaggatga atatcagaga tccacaccta gatatttcat 1800
 aatcaaagtg tcaaatgaca aagaatcttg aaagcagcaa gagatgagca 1850
 acttatcttg ttcaaaggat ctttgatcag attaacagct catttctcct 1900
 cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950
 aaccttcaac tgtaattatt ggacttttga gtcttagatg gtcttgacct 2000
 ctttgtcttc agggacagtt tttcaattta atccctaata acaattagtc 2050
 aagcttcctt gacctgtagg aaggcctgtc tttaggccgg gcacagtggc 2100
 ttacacctgt aatcccagca ctttgggagg ccagacggg tggatcattt 2150
 ggggtcaggc tgatctcaaa ctctgagtt caggtgatct gccgcctca 2200
 gcctccaaa gtgttgatg tgcaggcgtg agccactgag cctggccgga 2250
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 gtgatcccaa gtagcttga ttgtaaacat gcaccacat gcctggctaa 2350
 tttttgtatt ttagtagag acgtgttagc caggtggtc tcgatctcct 2400
 gacctcaagt gaccacctgc ctacgcctcc caaagtactg ggattacagg 2450
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ttgttctgtt gccagggctg gagtacagtg gcacagtctt ggctcactgc 2650
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 agctgtatatt ttttgtatatt tgtattttgt agctgtagtt tttgtatatt 2750
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 agctcaagtg atctgcctgc ttcagcctcc caaagtgctg ggattacaga 2850
 catgagccac tgcacctggc aaactcccaa aattcaacac acacacacaa 2900
 aaaaccacct gattcaaaat gggcagaggg gccgggtgtg gcccacaacta 2950
 ccaggagagac tgaagtggga ggatcgcttg ggcattgagaa gtcgaggctg 3000
 cagtgaagtcg aggttgtgctg actgcattcc agcctggaca acagagtga 3050
 accctgtctc 3060

<210> 297
 <211> 368
 <212> PRT
 <213> Homo sapiens

<400> 297
 Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu
 1 5 10 15
 Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe
 20 25 30
 Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu
 35 40 45
 Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln
 50 55 60
 Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu
 65 70 75
 Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala
 80 85 90
 Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly
 95 100 105
 Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val
 110 115 120
 Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr
 125 130 135
 Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu
 140 145 150
 Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr
 155 160 165

Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe
170 175 180

Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala Lys
185 190 195

Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly
200 205 210

Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val
215 220 225

Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu
230 235 240

Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val
245 250 255

Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala
260 265 270

Ala Gln Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln
275 280 285

Glu Ile Tyr Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys
290 295 300

Pro Ala Arg Arg Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala
305 310 315

Thr Ile Leu Leu Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe
320 325 330

Ala Ser Gly Ser Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val
335 340 345

Gly Ala Ala Ser Phe Gly Val Arg Arg Leu Ile Gly Glu Ser Leu
350 355 360

Glu Pro Gly Arg Trp Arg Leu Gln
365

<210> 298
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 298
cttcctctgt ggggtggacca tgtg 24

<210> 299
<211> 21
<212> DNA

agggtcaagg gcattgctgt gcctgccagg tatagtgcct acatgtggtg 800
 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850
 aaatctctca gttcaccaga tgggtgtagg cccagcattg taaattcaca 900
 cgttgactgt gcttgtgaat tatctgggga tgcaggctct gattcagtag 950
 gcccagggtt ggcattctcta acaaactccc acgtgatgct gatgctggtc 1000
 ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050
 tggctcacac ctatgatccc agcacttttg gaggctgagg caggctgata 1100
 acctggagtc aggatttcaa gactagcctg gccaacatgg tggaacccca 1150
 tctgtactaa aaatacacia attagctggg catggtggca catgcctgta 1200
 gtcccagcta cttgggaggg tgaagcaaga gaatcgcttg aacctgggag 1250
 gcgagggttg cagtgagccg agatcaggcc actgtattcc aaccagggtg 1300
 acagagtgag actctatgtc caaaaaaaaa aaaa 1334

<210> 302
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 302
 Met His His Ser Leu Gln Cys Pro Gly Ala Ala Thr Arg His Ile
 1 5 10 15
 His Leu Cys Val Cys Phe Ser Phe Ala Leu Ala Leu Gly His Phe
 20 25 30
 Leu Leu Ile Ser Leu Val Gly Lys Gly Leu Ser Leu Ser Cys Gly
 35 40 45
 Val Gly Gly Arg Gln Ala Gly Leu Arg Leu Ile Arg Pro Trp Val
 50 55 60
 Arg Arg Glu Gly Lys Ile Asn Phe Tyr Thr Asn Gly Asp Ser Trp
 65 70 75
 Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr
 80 85 90
 Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln
 95 100 105
 Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu
 110 115 120
 Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr
 125 130 135
 Cys Gly Val Leu Leu Ser Phe Leu

140

<210> 303
<211> 1768
<212> DNA
<213> Homo sapiens

<400> 303
ggctggactg gaactcctgg tcccaagtga tccacccgcc tcagcctccc 50
aagggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac 100
tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150
tatgctgtgg tggctagtgc tctactcct acctacatta aaatctgttt 200
tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250
ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300
ttctaccac accgtccct cgaagccggg gacagcctca ccttgctggc 350
ctctcgctgg agcagtgcc tcaccaactg tctcacgtct ggaggcactg 400
actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg 450
tgggccttgc cctggccgta gaagggattg acaagccga agatttcata 500
ggcgatggct cccactgccc aggcacagc cttgctgtag tcaatcactg 550
ccctggggcc aggacggg ccgtggacac gctcagaagc agtgggtgag 600
acatcacgct gcccgccat ctaacctttt catgtcctgc acatcacctg 650
atccatgggc taatctgaac tctgtcccaa ggaaccaga gcttgagtga 700
gctgtggctc agaccagaa ggggtctgct tagaccacct ggtttatgtg 750
acaggacttg cattctcctg gaacatgagg gaacgccgga ggaaagcaa 800
gtggcaggga aggaacttgt gccaaattat gggtcagaaa agatggaggt 850
gttgggttat cacaaggcat cgagtctcct gcattcagt gacatgtggg 900
ggaagggctg ccgatggcg atgacacact cgggactcac ctctggggcc 950
atcagacagc cgtttccgcc ccgatccacg taccagctgc tgaagggcaa 1000
ctgcaggccg atgtctctat cagccaggca gcagccaaaa tctgcgatca 1050
ccagccaggg gcagccgtct gggaaggagc aagcaaagt accatttctc 1100
ctccctcct tccctctgag aggcctcct atgtccctac taaagccacc 1150
agcaagacat agctgacagg ggctaattgg tcagtgttgg ccagggaggt 1200
cagcaaggcc tgagagctga tcagaaggc ctgctgtgcg aacacggaaa 1250

tgctccagc aagcacaggc tgcaaaatcc ccaggcaaag gactgtgtgg 1300
 ctcaatttaa atcatgttct agtaattgga gctgtcccca agaccaaagg 1350
 agctagagct tgggttcaaat gatctccaag ggcccttata cccaggaga 1400
 ctttgatttg aatttgaaac cccaaatcca aacctaagaa ccagggtgcat 1450
 taagaatcag ttattgccgg gtgtggtggc ctgtaatgcc aacatttttg 1500
 gaggccgagg cgggtagatc acctgaggtc aggagttcaa gaccagcctg 1550
 gccaacatgg tgaaaccctt gtctctacta aaaatacaaa aaaactagcc 1600
 aggcatggtg gtgtgtgcct gtatcccgag tactcgggag gctgagacag 1650
 gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700
 ttcagcctga gcaacacagc gagactctgt ctcagaaaaa ataaaaaaag 1750
 aattatgggtt atttgtaa 1768

<210> 304
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 304
 Met Leu Trp Trp Leu Val Leu Leu Leu Leu Pro Thr Leu Lys Ser
 1 5 10 15
 Val Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu
 20 25 30
 Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly
 35 40 45
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly
 50 55 60
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro
 65 70 75
 Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala
 80 85 90
 Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly
 95 100 105
 Arg Arg Arg Asp

<210> 305
 <211> 989
 <212> DNA
 <213> Homo sapiens

<400> 305

gcggggcccg	gagtgccgaga	cctgtcccag	gagctccagc	tcacgtgacc	50
tgtcactgcc	tcccgccgcc	tcctgcccgc	gccatgaccc	agccggtgcc	100
ccggctctcc	gtgcccgcg	cgctggccct	gggctcagcc	gcactgggcg	150
ccgccttcgc	cactggcctc	ttcctgggga	ggcggtgccc	cccatggcga	200
ggccggcgag	agcagtgcct	gcttcccccc	gaggacagcc	gcctgtggca	250
gtatcttctg	agccgctcca	tgcgggagca	ccgggcgctg	cgaagcctga	300
ggctgctgac	cctggagcag	ccgcaggggg	attctatgat	gacctgcgag	350
caggcccagc	tcttgccaa	cctggcgcg	ctcatccagg	ccaagaaggc	400
gctggacctg	ggcaccttca	cgggctactc	cgccctggcc	ctggccctgg	450
cgctgcccgc	ggacggggcg	gtggtgacct	gcgaggtgga	cgcgagccc	500
ccggagctgg	gacggcccct	gtggaggcag	gccgaggcgg	agcacaagat	550
cgacctccgg	ctgaagcccg	ccttgagagc	cctggacgag	ctgctggcgg	600
cgggcgaggc	cggcaccttc	gacgtggccg	tggtggatgc	ggacaaggag	650
aactgctccg	cctactacga	gcgctgcctg	cagctgctgc	gacccggagg	700
catcctcgcc	gtcctcagag	tcctgtggcg	cgggaagggtg	ctgcaacctc	750
cgaaagggga	cgtaggcggc	gagtgtgtgc	gaaacctaaa	cgaacgcata	800
cggcgggacg	tcagggtcta	catcagcctc	ctgcccctgg	gcgatggact	850
caccttggcc	ttcaagatct	agggctggcc	cctagtgagt	gggctcgagg	900
gagggttgcc	tgggaacccc	aggaattgac	cctgagtttt	aaattcgaaa	950
ataaagtggg	gctgggacac	aaaaaaaaaa	aaaaaaaaaa	989	

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<210> 306
<211> 262
<212> PRT
<213> Homo sapiens
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<400> 306
Met Thr Gln Pro Val Pro Arg Leu Ser Val Pro Ala Ala Leu Ala
  1          5          10          15

Leu Gly Ser Ala Ala Leu Gly Ala Ala Phe Ala Thr Gly Leu Phe
          20          25          30

Leu Gly Arg Arg Cys Pro Pro Trp Arg Gly Arg Arg Glu Gln Cys
          35          40          45

Leu Leu Pro Pro Glu Asp Ser Arg Leu Trp Gln Tyr Leu Leu Ser
          50          55          60

```

Arg Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu
65 70 75

Thr Leu Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln
80 85 90

Ala Gln Leu Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys
95 100 105

Ala Leu Asp Leu Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu
110 115 120

Ala Leu Ala Leu Pro Ala Asp Gly Arg Val Val Thr Cys Glu Val
125 130 135

Asp Ala Gln Pro Pro Glu Leu Gly Arg Pro Leu Trp Arg Gln Ala
140 145 150

Glu Ala Glu His Lys Ile Asp Leu Arg Leu Lys Pro Ala Leu Glu
155 160 165

Thr Leu Asp Glu Leu Leu Ala Ala Gly Glu Ala Gly Thr Phe Asp
170 175 180

Val Ala Val Val Asp Ala Asp Lys Glu Asn Cys Ser Ala Tyr Tyr
185 190 195

Glu Arg Cys Leu Gln Leu Leu Arg Pro Gly Gly Ile Leu Ala Val
200 205 210

Leu Arg Val Leu Trp Arg Gly Lys Val Leu Gln Pro Pro Lys Gly
215 220 225

Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu Arg Ile Arg
230 235 240

Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly Asp Gly
245 250 255

Leu Thr Leu Ala Phe Lys Ile
260

<210> 307
<211> 2272
<212> DNA
<213> Homo sapiens

<400> 307
ccgccgccgc agccgctacc gccgctgcag ccgctttccg cggcctgggc 50
ctctcgccgt cagcatgccca cagccttca agcccgggga cttggtgttc 100
gctaagatga agggctaccc tcactggcct gccaggatcg acgacatcgc 150
ggatggcgcc gtgaagcccc caccacaaca gtaccccatc tttttctttg 200
gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250

aaatgtaaag acaagtacgg gaagcccaac aagaggaaag gcttcaatga 300
 agggctgtgg gagatccaga acaacccccca cgccagctac agcgcccctc 350
 cgccagtggg ctctccgac agcgaggccc ccgaggccaa ccccgccgac 400
 ggcagtggcg ctgacgagga cgatgaggac cgggggggtca tggccgtcac 450
 agcggtaacc gccacagctg ccagcgacag gatggagagc gactcagact 500
 cagacaagag tagcgacaac agtggcctga agaggaagac gcctgcgcta 550
 aagatgtc⁰gg tctcgaaacg agcccgaaag gcctccagcg acctggatca 600
 ggccagcgtg tccccatccg aagaggagaa ctcggaagc tcattctgagt 650
 cggagaagac cagcgaccag gacttcacac ctgagaagaa agcagcggtc 700
 cgggcgccac ggagggggccc tctgggggga cggaaaaaaa agaaggcgcc 750
 gtcagcctcc gactccgact ccaaggccga ttcgacggg gccaaagcctg 800
 agccggtggc catggcgcgg tcggcgctct cctcctctc ttctcctcc 850
 tctcctgact ccgatgtgtc tgtgaagaag cctccgaggg gcaggaagcc 900
 agcggagaag cctctccga agccgcgagg gcggaaaccg aagcctgaac 950
 ggcctccgtc cagctccagc agtgacagt acagcgacga ggtggaccgc 1000
 atcagtgagt ggaagcggcg ggacgaggcg cggaggcgcg agctggaggc 1050
 ccggcgggcg cgagagcagg aggaggagct gcggcgctg cgggagcagg 1100
 agaaggagga gaaggagcgg aggcgcgagc gggccgaccg cggggagggt 1150
 gagcggggca gcggcgggag cagcggggac gagctcaggg aggacgatga 1200
 gcccgtcaag aagcggggac gcaagggccg gggccggggg cccccgtct 1250
 cctctgactc cgagcccag gccgagctgg agagagaggc caagaaatca 1300
 gcgaagaagc cgcagtcctc aagcacagag cccgccagga aacctggcca 1350
 gaaggagaag agagtgcggc ccgaggagaa gcaacaagcc aagcccgtga 1400
 aggtggagcg gacccggaag cggtcgagg gcttctcgat ggacaggaag 1450
 gtagagaaga agaaagagcc ctccgtggag gagaagctgc agaagctgca 1500
 cagtgagatc aagtttgccc taaaggctga cagcccggaac gtgaagaggt 1550
 gcctgaatgc cctagaggag ctgggaaccc tgcaggtgac ctctcagatc 1600
 ctccagaaga acacagacgt ggtggccacc ttgaagaaga ttgcgcgtta 1650
 caaagcgaac aaggacgtaa tggagaaggc agcagaagtc tatacccggc 1700

tcaagtcgcg ggtcctcggc ccaaagatcg aggcggtgca gaaagtgaac 1750
aaggctggga tggagaagga gaaggccgag gagaagctgg ccggggagga 1800
gctggccggg gaggaggccc ccaggagaa ggcggaggac aagcccagca 1850
ccgatctctc agccccagtg aatggcgagg ccacatcaca gaagggggag 1900
agcgcagagg acaaggagca cgaggagggt cgggactcgg aggaggggcc 1950
aaggtgtggc tcctctgaag acctgcacga cagcgtacgg gaggggtccc 2000
acctggacag gcctgggagc gaccggcagg agcgcgagag ggcacggggg 2050
gactcggagg ccctggacga ggagagctga gccgcgggca gccaggccca 2100
gccccgccc gagctcaggc tgccctctc cttccccggc tcgcaggaga 2150
gcagagcaga gaactgtggg gaacgctgtg ctgtttgtat ttgttccctt 2200
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<210> 308
<211> 671
<212> PRT
<213> Homo sapiens

<400> 308
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35 40 45
Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro
50 55 60
Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys
65 70 75
Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala
80 85 90
Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala
95 100 105
Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp
110 115 120
Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala
125 130 135
Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Ser Asp Lys Ser Ser

	140		145		150
Asp Asn Ser Gly	Leu 155	Lys Arg Lys Thr	Pro 160	Ala Leu Lys Met	Ser 165
Val Ser Lys Arg	Ala 170	Arg Lys Ala Ser	Ser 175	Asp Leu Asp Gln	Ala 180
Ser Val Ser Pro	Ser 185	Glu Glu Glu Asn	Ser 190	Glu Ser Ser Ser	Glu 195
Ser Glu Lys Thr	Ser 200	Asp Gln Asp Phe	Thr 205	Pro Glu Lys Lys	Ala 210
Ala Val Arg Ala	Pro 215	Arg Arg Gly Pro	Leu 220	Gly Gly Arg Lys	Lys 225
Lys Lys Ala Pro	Ser 230	Ala Ser Asp Ser	Asp 235	Ser Lys Ala Asp	Ser 240
Asp Gly Ala Lys	Pro 245	Glu Pro Val Ala	Met 250	Ala Arg Ser Ala	Ser 255
Ser Ser Ser Ser	Ser 260	Ser Ser Ser Ser	Asp 265	Ser Asp Val Ser	Val 270
Lys Lys Pro Pro	Arg 275	Gly Arg Lys Pro	Ala 280	Glu Lys Pro Leu	Pro 285
Lys Pro Arg Gly	Arg 290	Lys Pro Lys Pro	Glu 295	Arg Pro Pro Ser	Ser 300
Ser Ser Ser Asp	Ser 305	Asp Ser Asp Glu	Val 310	Asp Arg Ile Ser	Glu 315
Trp Lys Arg Arg	Asp 320	Glu Ala Arg Arg	Arg 325	Glu Leu Glu Ala	Arg 330
Arg Arg Arg Glu	Gln 335	Glu Glu Glu Leu	Arg 340	Arg Leu Arg Glu	Gln 345
Glu Lys Glu Glu	Lys 350	Glu Arg Arg Arg	Glu 355	Arg Ala Asp Arg	Gly 360
Glu Ala Glu Arg	Gly 365	Ser Gly Gly Ser	Ser 370	Gly Asp Glu Leu	Arg 375
Glu Asp Asp Glu	Pro 380	Val Lys Lys Arg	Gly 385	Arg Lys Gly Arg	Gly 390
Arg Gly Pro Pro	Ser 395	Ser Ser Asp Ser	Glu 400	Pro Glu Ala Glu	Leu 405
Glu Arg Glu Ala	Lys 410	Lys Ser Ala Lys	Lys 415	Pro Gln Ser Ser	Ser 420
Thr Glu Pro Ala	Arg 425	Lys Pro Gly Gln	Lys 430	Glu Lys Arg Val	Arg 435

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Pro Glu Glu Lys Gln Gln Ala Lys Pro Val Lys Val Glu Arg Thr
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Arg Lys Arg Ser Glu Gly Phe Ser Met Asp Arg Lys Val Glu Lys
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Lys Lys Glu Pro Ser Val Glu Glu Lys Leu Gln Lys Leu His Ser
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Glu Ile Lys Phe Ala Leu Lys Val Asp Ser Pro Asp Val Lys Arg
485                               490                               495

Cys Leu Asn Ala Leu Glu Glu Leu Gly Thr Leu Gln Val Thr Ser
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Gln Ile Leu Gln Lys Asn Thr Asp Val Val Ala Thr Leu Lys Lys
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Ile Arg Arg Tyr Lys Ala Asn Lys Asp Val Met Glu Lys Ala Ala
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Glu Val Tyr Thr Arg Leu Lys Ser Arg Val Leu Gly Pro Lys Ile
545                               550                               555

Glu Ala Val Gln Lys Val Asn Lys Ala Gly Met Glu Lys Glu Lys
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Ala Glu Glu Lys Leu Ala Gly Glu Glu Leu Ala Gly Glu Glu Ala
575                               580                               585

Pro Gln Glu Lys Ala Glu Asp Lys Pro Ser Thr Asp Leu Ser Ala
590                               595                               600

Pro Val Asn Gly Glu Ala Thr Ser Gln Lys Gly Glu Ser Ala Glu
605                               610                               615

Asp Lys Glu His Glu Glu Gly Arg Asp Ser Glu Glu Gly Pro Arg
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Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu Gly Pro
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Asp Leu Asp Arg Pro Gly Ser Asp Arg Gln Glu Arg Glu Arg Ala
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Arg Gly Asp Ser Glu Ala Leu Asp Glu Glu Ser
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<210> 309
<211> 3871
<212> DNA
<213> Homo sapiens

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 ggatattata ttcaaactag acacacataa tttggagtct ggcagactga 650
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 tacctctact ctggaacagc ttctgatttc cttggcaaag atactgcatt 750
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 ataccagaca cctacaatcc agatgatgat aaaatatatt tcttctttcg 900
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<210> 310
 <211> 777
 <212> PRT
 <213> Homo sapiens

<400> 310
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 20 25 30
 Phe Leu Pro Val Thr Gly Thr Leu Lys Gln Asn Ile Pro Arg Leu
 35 40 45
 Lys Leu Thr Tyr Lys Asp Leu Leu Leu Ser Asn Ser Cys Ile Pro
 50 55 60
 Phe Leu Gly Ser Ser Glu Gly Leu Asp Phe Gln Thr Leu Leu Leu
 65 70 75
 Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

80										85					90				
Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile					
				95					100					105					
Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala					
				110					115					120					
Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu					
				125					130					135					
Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala					
				140					145					150					
Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu					
				155					160					165					
Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg					
				170					175					180					
Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met					
				185					190					195					
Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly					
				200					205					210					
Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His					
				215					220					225					
His	Tyr	Ile	Arg	Thr	Asp	Ile	Ser	Glu	His	Tyr	Trp	Leu	Asn	Gly					
				230					235					240					
Ala	Lys	Phe	Ile	Gly	Thr	Phe	Phe	Ile	Pro	Asp	Thr	Tyr	Asn	Pro					
				245					250					255					
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Arg	Glu	Ser	Ser	Gln	Glu					
				260					265					270					
Gly	Ser	Thr	Ser	Asp	Lys	Thr	Ile	Leu	Ser	Arg	Val	Gly	Arg	Val					
				275					280					285					
Cys	Lys	Asn	Asp	Val	Gly	Gly	Gln	Arg	Ser	Leu	Ile	Asn	Lys	Trp					
				290					295					300					
Thr	Thr	Phe	Leu	Lys	Ala	Arg	Leu	Ile	Cys	Ser	Ile	Pro	Gly	Ser					
				305					310					315					
Asp	Gly	Ala	Asp	Thr	Tyr	Phe	Asp	Glu	Leu	Gln	Asp	Ile	Tyr	Leu					
				320					325					330					
Leu	Pro	Thr	Arg	Asp	Glu	Arg	Asn	Pro	Val	Val	Tyr	Gly	Val	Phe					
				335					340					345					
Thr	Thr	Thr	Ser	Ser	Ile	Phe	Lys	Gly	Ser	Ala	Val	Cys	Val	Tyr					
				350					355					360					
Ser	Met	Ala	Asp	Ile	Arg	Ala	Val	Phe	Asn	Gly	Pro	Tyr	Ala	His					
				365					370					375					

[illegible]

$\frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) e^{-x^2} dx = \frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) e^{-x^2} dx$

				665					670					675
Ile	Val	Lys	Leu	Thr 680	Leu	Asn	Val	Ile	Glu 685	Asn	Glu	Gln	Met	Glu 690
Asn	Thr	Gln	Arg	Ala 695	Glu	His	Glu	Glu	Gly 700	Gln	Val	Lys	Asp	Leu 705
Leu	Ala	Glu	Ser	Arg 710	Leu	Arg	Tyr	Lys	Asp 715	Tyr	Ile	Gln	Ile	Leu 720
Ser	Ser	Pro	Asn	Phe 725	Ser	Leu	Asp	Gln	Tyr 730	Cys	Glu	Gln	Met	Trp 735
His	Arg	Glu	Lys	Arg 740	Arg	Gln	Arg	Asn	Lys 745	Gly	Gly	Pro	Lys	Trp 750
Lys	His	Met	Gln	Glu 755	Met	Lys	Lys	Lys	Arg 760	Asn	Arg	Arg	His	His 765
Arg	Asp	Leu	Asp	Glu 770	Leu	Pro	Arg	Ala	Val 775	Ala	Thr			

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<210> 311
<211> 25
<212> DNA
<213> Artificial
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<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.
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<400> 311
caacgcagcc gtgataaaca agtgg 25
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```
<210> 312
<211> 24
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.
```

```
<400> 312
gcttggacat gtaccaggcc gtqg 24
```

```
<210> 313
<211> 45
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.
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<400> 313
ggccagactg atttgctcaa ttcctggaag tgatggggca gatac 45

<210> 314
<211> 3934
<212> DNA
<213> Homo sapiens

<400> 314
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gagcatgccc accgcgggga gcagacaacc tcccaggtaa gctgggagca 100
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304

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 tttcttgtct ttatctaata aactcaatat taag 3934

<210> 315
 <211> 370
 <212> PRT
 <213> Homo sapiens

<400> 315
 Met Gln Leu Ala Lys Tyr Gln Ser His Ser Lys Ser Cys Pro Thr
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Val	Phe	Pro	Pro	Thr	Pro	Val	Leu	Cys	Leu	Pro	Asn	Gln	Val	Leu	20	25	30
Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala	35	40	45
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg	50	55	60
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu	65	70	75
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala	80	85	90
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser	95	100	105
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp	110	115	120
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu	125	130	135
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro	140	145	150
Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp	155	160	165
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu	170	175	180
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu	185	190	195
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser	200	205	210
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu	215	220	225
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln	230	235	240
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu	245	250	255
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly	260	265	270
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu	275	280	285
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu	290	295	300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala			

305 310 315
Pro Thr Ser Val Leu Asp Gly Pro Pro Ala Pro Val Leu Pro Gly
320 325 330
Asp Lys Ala Leu Asp Phe Pro Gly Phe Leu Asp Met Met Ala Pro
335 340 345
Arg Leu Arg Pro Met Arg Pro Pro Pro Pro Pro Ala Lys Ala
350 355 360
Pro Asp Pro Gly His Pro Asp Pro Leu Thr
365 370

<210> 316
<211> 4407
<212> DNA
<213> Homo sapiens

<400> 316
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<210> 317
<211> 837
<212> PRT
<213> Homo sapiens

<400> 317
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Trp Leu Trp Gly Ala Gln Pro Cys Leu Leu Leu Pro Ile Val Pro
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Leu Ser Trp Leu Val Trp Leu Leu Leu Leu Leu Ala Ser Leu
35 40 45
Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu
50 55 60
Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser
65 70 75
Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu
80 85 90
Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu
95 100 105
Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly
110 115 120
Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp
125 130 135
Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu

Gly Val Leu Gln Tyr Arg Gly Ala Glu	Leu His Leu Gln Pro Leu	140	145	150
155	160	165		
Glu Gly Gly Thr Pro Asn Ser Ala Gly	Gly Pro Gly Ala His Ile	170	175	180
185	190	195		
Leu Arg Arg Lys Ser Pro Ala Ser Gly	Gln Gly Pro Met Cys Asn	200	205	210
215	220	225		
Val Lys Ala Pro Leu Gly Ser Pro Ser	Pro Arg Pro Arg Arg Ala	230	235	240
245	250	255		
Lys Arg Phe Ala Ser Leu Ser Arg Phe	Val Glu Thr Leu Val Val	260	265	270
275	280	285		
Ala Asp Asp Lys Met Ala Ala Phe His	Gly Ala Gly Leu Lys Arg	290	295	300
305	310	315		
Tyr Leu Leu Thr Val Met Ala Ala Ala	Ala Lys Ala Phe Lys His	320	325	330
335	340	345		
Pro Ser Ile Arg Asn Pro Val Ser Leu	Val Val Thr Arg Leu Val	350	355	360
365	370	375		
Ile Leu Gly Ser Gly Glu Glu Gly Pro	Gln Val Gly Pro Ser Ala	380	385	390
395	400	405		
Ala Gln Thr Leu Arg Ser Phe Cys Ala	Trp Gln Arg Gly Leu Asn	410	415	420
425	430	435		
Thr Pro Glu Asp Ser Gly Pro Asp His	Phe Asp Thr Ala Ile Leu	440	445	450
455	460	465		
Phe Thr Arg Gln Asp Leu Cys Gly Val	Ser Thr Cys Asp Thr Leu	470	475	480
485	490	495		
Gly Met Ala Asp Val Gly Thr Val Cys	Asp Pro Ala Arg Ser Cys	500	505	510
515	520	525		
Ala Ile Val Glu Asp Asp Gly Leu Gln	Ser Ala Phe Thr Ala Ala	530	535	540
545	550	555		
His Glu Leu Gly His Val Phe Asn Met	Leu His Asp Asn Ser Lys	560	565	570
575	580	585		
Pro Cys Ile Ser Leu Asn Gly Pro Leu	Ser Thr Ser Arg His Val	590	595	600
605	610	615		
Met Ala Pro Val Met Ala His Val Asp	Pro Glu Glu Pro Trp Ser	620	625	630
635	640	645		
Pro Cys Ser Ala Arg Phe Ile Thr Asp	Phe Leu Asp Asn Gly Tyr	650	655	660
665	670	675		
Gly His Cys Leu Leu Asp Lys Pro Glu	Ala Pro Leu His Leu Pro	680	685	690
695	700	705		

725	730	735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp		
740	745	750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr		
755	760	765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro		
770	775	780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg		
785	790	795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro		
800	805	810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu		
815	820	825
Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys		
830	835	

<210> 318
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 318
 ccctgaagct gccagatggc tcc 23

<210> 319
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 319
 ctgtgctctt cggtgcagcc agtc 24

<210> 320
 <211> 43
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-43
 <223> Synthetic construct.

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<400> 320
ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321
<211> 1197
<212> DNA
<213> Homo sapiens

<400> 321
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gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100
ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150
ttgtggactg gtgtttggta tcctggccct aactctaatt gtcctgtttt 200
gggggagcaa gcacttctgg ccggaggtag ccaaaaaagc ctatgacatg 250
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300
tgatcctgtg accagaactg aaatattcag aagcggaaat ggcactgatg 350
aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400
gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450
atcttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500
ctttctttga acagtcagtg atttggttcc cagcagaaaa gcctattgaa 550
aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600
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actttgagga ggaggagaga gatcttcact ttcctgcaa cgaaaaaaaa 700
gggattgaac aaaatgaaca gtgggtgggc cctcaagtga aagtagagaa 750
gacccgtcac gccagacaag caagtgagga agaacttcca ataatgact 800
atactgaaaa tggaatagaa tttgatccca tgctggatga gagaggttat 850
tgttgtatct actgccgtcg aggcaaccgc tattgccgcc gcgtctgtga 900
acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950
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atataataaa tgcagctctat tcaatgaatt tctgcctatg aggcactctg 1100
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<210> 322

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<211> 317
 <212> PRT
 <213> Homo sapiens

<400> 322

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Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	20	25	30	
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	35	40	45	
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	50	55	60	
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	65	70	75	
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	80	85	90	
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	95	100	105	
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	110	115	120	
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	125	130	135	
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	140	145	150	
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	155	160	165	
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	170	175	180	
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	185	190	195	
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	200	205	210	
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	215	220	225	
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	230	235	240	
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	245	250	255	
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	260	265	270	

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
 275 280 285
 Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
 290 295 300
 Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
 305 310 315

Arg Val

<210> 323
 <211> 1174
 <212> DNA
 <213> Homo sapiens

<400> 323
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ataccaaaga ctgaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050
atatttatgt gggtgatttg ataacaagtt taatataaag tgacttgga 1100
gtttggtcag tgggggttggg ttgtgatcca ggaataaacc ttgcggatgt 1150
ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324
<211> 239
<212> PRT
<213> Homo sapiens

<400> 324
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Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp
20 25 30
Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser
35 40 45
Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly
50 55 60
Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln
65 70 75
Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu
80 85 90
Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr
95 100 105
Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu
110 115 120
Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala
125 130 135
Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro
140 145 150
Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr
155 160 165
Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu
170 175 180
Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln
185 190 195
Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala
200 205 210
Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val
215 220 225

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
230 235

<210> 325
<211> 2121
<212> DNA
<213> Homo sapiens

<400> 325
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gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac 200
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80										85					90				
Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg					
				95					100					105					
Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr					
				110					115					120					
Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly					
				125					130					135					
Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser					
				140					145					150					
Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val					
				155					160					165					
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val					
				170					175					180					
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala					
				185					190					195					
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser					
				200					205					210					
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe					
				215					220					225					
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile					
				230					235					240					
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro					
				245					250					255					
Ser	Lys	His	Asp	Tyr	Val														
				260															

<210> 327
 <211> 2010
 <212> DNA
 <213> Homo sapiens

<400> 327
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 gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgtcggcctt 200
 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250
 tgaattgcgt gaggcaggct aacatcagga tgcagtgcaa aatctatgat 300
 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350

tgctgcttcc gtgatgtcct tcttggtttt catgatggcc atccttggca 400
 tgaaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt 450
 ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500
 ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550
 tagtgaatgt tgcccaaaaa cgtgagcttg gagaagctct ctacttagga 600
 tggaccacgg cactggtgct gattgttggg ggagctctgt tctgctgctg 650
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 caaagaaaact ttgatttaact gttcttaact gcctaattctt aattacagga 900
 actgtgcata agctatttat gattctataa gctatttcag cagaatgaga 950
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 taaggtgggt caagcatcta ctctttttat catttacttc aaaatgacat 1050
 tgctaaagac tgcattattt tactactgta atttctccac gacatagcat 1100
 tatgtacata gatgagtgtg acatttatat ctcatataga gacatgctta 1150
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 actcaactat tgctttttcag ggaaatcatg gatagggttg aagaaggtta 1250
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 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350
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atttttgttc tgtgaaaaat aaatttcctt cttgtaccat ttctgttttag 1850
 ttttactaaa atctgtaaat actgtatattt tctgttttatt ccaaatttga 1900
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 aatgaatgtg ttctatttgc tttatacatt tatattaata aattgtacat 2000
 ttttctaatt 2010

<210> 328
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 328
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 Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp
 20 25 30
 Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn
 35 40 45
 Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile
 50 55 60
 Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro
 65 70 75
 Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met
 80 85 90
 Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr
 95 100 105
 Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu
 110 115 120
 Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile
 125 130 135
 Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn
 140 145 150
 Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu
 155 160 165
 Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala
 170 175 180
 Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr
 185 190 195
 Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
 200 205 210

Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val
215 220 225

<210> 329

<211> 1315

<212> DNA

<213> Homo sapiens

<400> 329

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gaccgctttc atcggcaaca gcatcgtggt ggcccagggt gtgtgggagg 150
gcctgtggat gtcctgcgtg gtgcagagca ccggccagat gcagtgaag 200
gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
cctctgtgtc atcgccctcc ttgtggcctt gttcggcttg ctggtctacc 300
ttgtctggggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350
cgcttggtgc tcacctctgg gattgtcttt gtcattctcag gggctctgac 400
gctaataccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450
accccttggt ggctgaggcc caaaagcggg agctgggggc ctccctctac 500
ttgggctggg cggcctcagg ccttttgttg ctgggtgggg ggttgctgtg 550
ctgcacttgc cctcggggg ggtcccaggg cccagccat tacatggccc 600
gctactcaac atctgcccct gccatctctc gggggccctc tgagtaccct 650
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gagccatcca gaagtggcag tgcccaacag ctttgggatg ggttcgtacc 750
ttttgtttct gcctcctgct atttttcttt tgactgagga tatttaaaat 800
tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggctct 850
gctgtttctc acccttgat gatggagcca aagaggggat gctttgagat 900
tctggatctt gacatgccca tcttagaagc cagtcaagct atggaactaa 950
tgcgagggt gcttgctgtg ctggcttgc aacaagacag actgtcccca 1000
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gctgcccccc atcctactca ggtctctgga gtcctctct tcacccctgg 1100
aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150
cctctgtttc ctccgtctg ataagacgtc cccccccag ggccagggtcc 1200
cagctatgta gacccccgcc cccacctcca aactgcacc cttctgccct 1250

tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met Ala Ser Ala Gly Met Gln Ile Leu Gly Val Val Leu Thr Leu
1 5 10 15

Leu Gly Trp Val Asn Gly Leu Val Ser Cys Ala Leu Pro Met Trp
20 25 30

Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val
35 40 45

Val Trp Glu Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly
50 55 60

Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln
65 70 75

Asp Leu Gln Ala Ala Arg Ala Leu Cys Val Ile Ala Leu Leu Val
80 85 90

Ala Leu Phe Gly Leu Leu Val Tyr Leu Ala Gly Ala Lys Cys Thr
95 100 105

Thr Cys Val Glu Glu Lys Asp Ser Lys Ala Arg Leu Val Leu Thr
110 115 120

Ser Gly Ile Val Phe Val Ile Ser Gly Val Leu Thr Leu Ile Pro
125 130 135

Val Cys Trp Thr Ala His Ala Ile Ile Arg Asp Phe Tyr Asn Pro
140 145 150

Leu Val Ala Glu Ala Gln Lys Arg Glu Leu Gly Ala Ser Leu Tyr
155 160 165

Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu Gly Gly Gly Leu
170 175 180

Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly Pro Ser His
185 190 195

Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser Arg Gly
200 205 210

Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val
215 220

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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 ttctacatct tgagcatctt ctaccactcc gaattgaacc agtcttcaaa 100
 gtaaaggcaa tggcatttta tcccttgcaa attgctgggc tggttcttgg 150
 gttccttggc atgggtggga ctcttgccac aaccttctg cctcagtgg 200
 ggagtatcag cttttgttgg cagcaacatt attgtctttg agaggctctg 250
 ggaagggctc tggatgaatt gcatccgaca agccagggtc cggttgcaat 300
 gcaagttcta tagctccttg ttggctctcc cgctgcctt ggaaacagcc 350
 cgggccctca tgtgtgtggc tgttgetctc tccttgatcg ccctgcttat 400
 tggcatctgt ggcatgaagc aggtccagtg cacaggctct aacgagaggg 450
 ccaaagcata ccttctggga acttcaggag tcctcttcat cctgacgggt 500
 atcttcgttc tgattccggt gagctggaca gccaatataa tcatcagaga 550
 tttctacaac ccagccatcc acataggtca gaaacgagag ctgggagcag 600
 cacttttctt tggctgggca agcgtctgtg tcctcttcat tggaggggggt 650
 ctgctttgtg gatcttctg ctgcaacaga aagaagcaag ggtacagata 700
 tccagtgcct ggctaccgtg tgccacacac agataagcga agaaatacga 750
 caatgcttag taagacctcc accagttatg tctaatagcct ccttttggct 800
 ccaagtatgg actatggtca atgtttttta taaagtcttg ctagaaactg 850
 taagtatgtg aggaggaga acttgcttta tgtctagatt tacattgata 900
 cgaaagtctc aatttggtac tgggtgtagg aatgaaaatg acttacttgg 950
 acattctgac ttcaggtgta ttaaatacat tgactattgt tggaccaat 1000
 cgctgtcca attttcatat tctaaattca agtataacca taatcattag 1050
 caagtgtaca atgatggact acttattact ttttgacat catgtattat 1100
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<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

1	5	10	15
Tyr Ser Ser Leu Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg	20	25	30
Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu	35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn	50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe	65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala	80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly	95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser	110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys	125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly	140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu	155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val	170		

<210> 333
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 333
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 atcactgggg gtctccttct gctctgtaca gtggtctatt tctgtagcag 100
 ctcaagaagct gctagtctgt ctcaaaaaaa agtggactgc agcattttaca 150
 agaagtatcc agtgggtggcc atcccctgcc ccatcacata cctaccagtt 200
 tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250
 gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300
 aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350
 tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400
 ggtgggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500

tttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr
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Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
20 25 30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
35 40 45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
50 55 60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
65 70 75

Arg Val Gln Phe Leu His Asp Gly Ser Cys
80 85

<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

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tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccaggt 150

ggcataagtg gaaataaaact caagctgatg cttcaaaaac gagaagcacc 200

tggtccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250

tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300

cccagaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350

agcgaaatth gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450

gcaattggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500

ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaat 550

agcgattctc ttcattgtatc tcctaattgcc ttacactact tggttttctga 600

ttgtctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
 gaagagttaa aacaacacat gtaaatgcct tttgatattt catgggaatg 700
 cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 336
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 1 5 10 15
 Leu Ala Leu Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
 20 25 30
 Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
 35 40 45
 Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
 50 55 60
 Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
 65 70 75
 Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
 80 85 90
 Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
 95 100 105
 Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
 110 115 120
 Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
 125 130 135
 Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
 140 145

<210> 337
 <211> 1310
 <212> DNA
 <213> Homo sapiens

<400> 337
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 tgaaggggtg ggtgatgagg tgaccgtcct tttctcgtg cttgcctgcc 150
 ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200
 gaccactgc ccagccgctc agggacccca acgccatccc agcccagcgc 250

agccatggca	gctaccgaca	gcatgagagg	ggaggcccca	ggggcagaga	300
ccccagcct	gagacacaga	ggtcaagctg	cacagccaga	gcccagcacg	350
gggttcacag	caacaccgcc	agccccggac	tccccgcagg	agcccctcgt	400
gctacggctg	aaattcctca	atgattcaga	gcagggtggc	agggcctggc	450
cccacgacac	cattgggtcc	ttgaaaagga	cccagtttcc	cggccgggaa	500
cagcaggtgc	gactcatcta	ccaagggcag	ctgctaggcg	acgacacca	550
gaccctgggc	agccttcacc	tccctcccaa	ctgcgttctc	cactgccacg	600
tgtccacgag	agtcggtccc	ccaaatcccc	cctgcccgcc	ggggtccgag	650
cccggcccc	ccgggctgga	aatcggcagc	ctgctgctgc	ccctgctgct	700
cctgctgttg	ctgctgctct	ggtactgcc	gatccagtac	cggcccttct	750
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ctgcctgccc	aggcccgcc	ctccggcctg	cctcttcccg	ctgccctgga	950
gcccagccct	gcgcgcgaga	ggactcccgg	gactggcgga	ggccccgccc	1000
tgcgaccgcc	ggggctcggg	gccacctccc	ggggctgctg	aacctcagcc	1050
cgcaactggga	gtgggctcct	cggggtcggg	catctgctgt	cgctgcctcg	1100
gccccgggca	gagccggggc	gccccggggg	cccgtcttag	tgttctgccg	1150
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acgccaggtc	ggtgggaggc	tggtgaaggg	gagcggggag	gggcagagga	1250
gttccccgga	acccgtgcag	attaaagtaa	ctgtgaagtt	ttaaaaaaaaa	1300
aaaaaaaaaa	1310				

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<210> 338
<211> 246
<212> PRT
<213> Homo sapiens
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<400> 338
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Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser
                20                25              30

Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly
                35                40              45

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Thr Pro Thr Pro Ser Gln Pro Ser Ala Ala Met Ala Ala Thr Asp
 50 55 60
 Ser Met Arg Gly Glu Ala Pro Gly Ala Glu Thr Pro Ser Leu Arg
 65 70 75
 His Arg Gly Gln Ala Ala Gln Pro Glu Pro Ser Thr Gly Phe Thr
 80 85 90
 Ala Thr Pro Pro Ala Pro Asp Ser Pro Gln Glu Pro Leu Val Leu
 95 100 105
 Arg Leu Lys Phe Leu Asn Asp Ser Glu Gln Val Ala Arg Ala Trp
 110 115 120
 Pro His Asp Thr Ile Gly Ser Leu Lys Arg Thr Gln Phe Pro Gly
 125 130 135
 Arg Glu Gln Gln Val Arg Leu Ile Tyr Gln Gly Gln Leu Leu Gly
 140 145 150
 Asp Asp Thr Gln Thr Leu Gly Ser Leu His Leu Pro Pro Asn Cys
 155 160 165
 Val Leu His Cys His Val Ser Thr Arg Val Gly Pro Pro Asn Pro
 170 175 180
 Pro Cys Pro Pro Gly Ser Glu Pro Gly Pro Ser Gly Leu Glu Ile
 185 190 195
 Gly Ser Leu Leu Leu Pro Leu Leu Leu Leu Leu Leu Leu Leu
 200 205 210
 Trp Tyr Cys Gln Ile Gln Tyr Arg Pro Phe Phe Pro Leu Thr Ala
 215 220 225
 Thr Leu Gly Leu Ala Gly Phe Thr Leu Leu Leu Ser Leu Leu Ala
 230 235 240
 Phe Ala Met Tyr Arg Pro
 245

<210> 339
 <211> 849
 <212> DNA
 <213> Homo sapiens

<400> 339
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 atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200
 tcaggccagc ctcacagtc gctgtgactt ggcccaggtg ctgcagctgg 250

aggacttggg tgggtttgag ggttactccc tgagtgactg gctgtgcctg 300
gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350
tggaagcttt gactatggcc tcttccagat caacagccac tactgggtgca 400
acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450
ctgctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500
gtccggagca cgggggatga acaactgggt agaatggagg ttgcactgtt 550
caggccggcc actctcctac tggctgacag gatgccgcct gagatgaaac 600
aggggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650
ggattcttca tttcttcttc ctactgcctc cacttcatgt tattttcttc 700
ccttcccatt tacaactaaa actgaccaga gcccaggaa taaatggttt 750
tcttggttcc ctccttactc ccatctggac ccagtcccct ggttcctgtc 800
tgttatttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340
<211> 148
<212> PRT
<213> Homo sapiens

<400> 340
Met Thr Lys Ala Leu Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala
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Leu Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val
20 25 30
Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser
35 40 45
Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser
50 55 60
Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe
65 70 75
Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser
80 85 90
Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn
95 100 105
Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala
110 115 120
Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly
125 130 135
Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 345

agcttttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346

<211> 2575

<212> DNA

<213> Homo sapiens

<400> 346

tctgacctga ctggaagcgt ccaaagaggg acggctgtca gccctgcttg 50
actgagaacc caccagctca tcccagacac ctcatagcaa cctattttata 100
caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150
aaggagaaaa ccggggtaaa gggaggggaag caattcaatt tgaagtcctt 200
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250
ggggtgaaac ttgggtcctg tggttttctg attgtaagtga gaagcagggtc 300
ttgcacacgc tgttggaaca tgtcaggacc aggttaagtga actggcagaa 350
aaacttccag gtggaacaag caacccatgt tctgctgcaa gcttgaagga 400
gcctggagcg ggagaaagct aacttgaaca tgacctgttg catttgga 450
gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500
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Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro
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Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg
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Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr
365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly
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Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly
395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln
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Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala
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Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu
470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu
485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His
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Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp
515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg
530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe

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Gly Ser Pro Gln His Leu Cys Phe Ala	Val Arg Gln Glu Gln Val	
560	565	570
Ile Leu Gln Asn Cys Thr Glu Glu Gly	Leu Ala Ile His Gln Gln	
575	580	585
His Trp Asp Phe Gln Glu Asn Gly Met	Ile Val His Ile Leu Ser	
590	595	600
Gly Lys Cys Met Glu Ala Val Val Gln	Glu Asn Asn Lys Asp Leu	
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<220>
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<220>
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<223> Synthetic construct.

<400> 349
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<220>
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<210> 351
 <211> 2524
 <212> DNA
 <213> Homo sapiens

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<210> 352
<211> 243
<212> PRT
<213> Homo sapiens
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35 40 45
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
50 55 60
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
65 70 75
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
95 100 105
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
110 115 120
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135
Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
140 145 150
Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
155 160 165
Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
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Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
185 190 195
Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
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Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
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Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
230 235 240

Leu Pro Lys

<210> 353
<211> 480
<212> DNA
<213> Homo sapiens

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<210> 354
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 354
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 35 40 45
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp
 50 55 60
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser
 65 70 75
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro
 80 85 90
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys
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 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala
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Ser

<210> 355
 <211> 2134
 <212> DNA
 <213> Homo sapiens

<400> 355
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<210> 356
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 356
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 20 25 30
 Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp
 35 40 45
 Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr
 50 55 60
 Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu
 65 70 75
 Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln
 80 85 90
 Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu
 95 100 105
 Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala
 110 115 120
 Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln
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 Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro

140

145

150

Ser Pro Arg Gly Asp Leu Pro
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<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

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<210> 358
 <211> 273
 <212> PRT
 <213> Homo sapiens

<400> 358
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 Ser Asp Gly Pro Gly Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp
 35 40 45
 Val Pro Ala Ala Met Glu Phe Ile Ala Ala Thr Glu Val Ala Val
 50 55 60
 Ile Gly Phe Phe Gln Asp Leu Glu Ile Pro Ala Val Pro Ile Leu
 65 70 75
 His Ser Met Val Gln Lys Phe Pro Gly Val Ser Phe Gly Ile Ser
 80 85 90
 Thr Asp Ser Glu Val Leu Thr His Tyr Asn Ile Thr Gly Asn Thr
 95 100 105
 Ile Cys Leu Phe Arg Leu Val Asp Asn Glu Gln Leu Asn Leu Glu
 110 115 120
 Asp Glu Asp Ile Glu Ser Ile Asp Ala Thr Lys Leu Ser Arg Phe
 125 130 135
 Ile Glu Ile Asn Ser Leu His Met Val Thr Glu Tyr Asn Pro Val
 140 145 150
 Thr Val Ile Gly Leu Phe Asn Ser Val Ile Gln Ile His Leu Leu
 155 160 165
 Leu Ile Met Asn Lys Ala Ser Pro Glu Tyr Glu Glu Asn Met His
 170 175 180
 Arg Tyr Gln Lys Ala Ala Lys Leu Phe Gln Gly Lys Ile Leu Phe
 185 190 195

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val Ile Ser
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Phe Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile Tyr
215 220 225
Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val
230 235 240
Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe Leu Ser Gly
245 250 255
Lys Leu Leu Lys Glu Asn Arg Glu Ser Glu Gly Lys Thr Pro Lys
260 265 270

Val Glu Leu

<210> 359
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 359
ccagcagtgccatactcca tagc 24

<210> 360
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.

<400> 360
tgacgagtgg gatacactgc 20

<210> 361
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 361
gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 362
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
ggagagccgc ggctgggacc ggagtgggga gcgcggcgctg gaggtgccac 50
ccggcgcggg tggcgagag atcagaagcc tcttcccaa gccgagccaa 100
cctcagcggg gacccgggct cagggacgcg gcggcgggcg cggcgactgc 150
agtggctgga cgatggcagc gtccgccgga gccggggcg tgattgcagc 200
cccagacagc cggcgctggc tgtggctcggg gctggcgggc gcgcttgggc 250
tcttgacagc tggagtatca gccttgggaag tatatacgcc aaaagaaatc 300
ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350
tagtacgact ggcgggttga cctcagcttc ctggagcttc cagccagagg 400
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450
cttggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag ttatacaca 550
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600
cctggacaca ttaggctcta tgtcgtagaa aaagagaatt tgctgtgtt 650
tccagtttgg gtagtggtgg gcatagttac tgctgtggc ctaggtctca 700
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800
gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850
tgccttctgg atctcaccag ggcccagtc tatatgcaca gttagaccac 900
tccggcggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950
tgcgatatc cgaaagaatt aagagaatac ctagaacata tctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050
atgtagcctt ggagaccag gcaaggacaa gtacacgtgt actcacagag 1100
ggagagaaag atgtgtacaa aggatatgta taaatattct atttagtcat 1150
cctgatatga ggagccagt ttgcatgatg aaaagatggg atgattctac 1200
atatgtaccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250
caattgggag atttcagaaa cattcctttc accatcattt agaaatgggt 1300
tgccttaatg gagacaatag cagatcctgt agtatttcca gtagacatgg 1350
ccttttaatc taagggttta agactgatta gtcttagcat ttactgtagt 1400
tggaggatgg agatgctatg atggaagcat acccaggggt gccttttagca 1450
cagtatcagt accatttatt tgtctgccgc ttttaaaaaa taccatttgg 1500
ctatgccact tgaaaacaat ttgagaagtt tttttgaagt ttttctcact 1550
aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600
tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650
attagcaaag gataaatgcc gaaggtcact tcattctgga cacagttgga 1700
tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750
cgtggagagt aaaaagtatc ggtttta 1777

<210> 364
<211> 269
<212> PRT
<213> Homo sapiens

<400> 364
Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp
1 5 10 15
Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu
20 25 30
Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu
35 40 45
Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe
50 55 60
Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser
65 70 75
Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr
80 85 90
Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp
95 100 105

cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550
gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600
ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgtcacaaca 650
agattactga tttcccatTT aagtggaatt cgtcattatg aaaaggacat 700
aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
gattttacta aattttaaac agagcaggag aatgaagcca aatgccggaa 850
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ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaattatt 1050
tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100
caggaagaaa acgagccagt gatttacaat agagcaaggt aaatgaatac 1150
cttctgctgt gtctagctat atcgcatctt aacactatTT tattaattaa 1200
aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacatttttg 1250
gagcttttct acatgtctgt tttctcatct gtaaagtga ggaagtaaaa 1300
catgtttata aagtaaaaaa a 1321

<210> 366
<211> 373
<212> PRT
<213> Homo sapiens

<400> 366
Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro
1 5 10 15
Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg
20 25 30
Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly
35 40 45
Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu
50 55 60
Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu
65 70 75
Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro
80 85 90

Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala
95 100 105

Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp
110 115 120

Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly
125 130 135

Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn
140 145 150

Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile
155 160 165

Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala
170 175 180

Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu
185 190 195

Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr
200 205 210

Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys
215 220 225

Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys
230 235 240

Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys
245 250 255

Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu
260 265 270

Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn
275 280 285

Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn
290 295 300

Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe
305 310 315

Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu
320 325 330

Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp
335 340 345

Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val
350 355 360

Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg
365 370

<210> 367

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100
ctggggcaac ccggtgctc ctgctcttgc tgatggcggt agcagcgccc 150
agtcgagccc ggggcagcgg ctgccggggc gggactggtg cgcgaggggc 200
tggggcgga ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250
tggagcactc atttgagatc gatgacagtg ccaacttccg gaagcggggc 300
tcaactgctc ggaaccagca ggatggtacc ttgtccctgt cacagcggca 350
gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400
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gaagctggtg gctatgtctc ctcttttgc cctgctgtgt ccttgggtga 500
gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550
tgggtgggct gtcggtggtg acgcaccccg ggggctgccg gggccatgag 600
gtggaggacg tggacctgga gctgttcaac acctcgggtg agctgcagcc 650
gcccaccaca gcccaggcc ctgagacggc ggccttcatt gagcgcctgg 700
agatggaaca ggcccagaag gccaagaacc cccaggagca gaagtccttc 750
ttcgccaaat actggatgta catcattccc gtcgtcctgt tcctcatgat 800
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ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950
agcttccagc agccaaaagc aactgttgtt ttggcaagac ggtcctgatg 1000
tacaagcttg attgaaattc actgctcact tgatacgtta ttcagaaacc 1050
caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100
ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372
<211> 269
<212> PRT
<213> Homo sapiens

<400> 372
Met Ala Ala Ala Ser Ala Gly Ala Thr Arg Leu Leu Leu Leu Leu
1 5 10 15
Leu Met Ala Val Ala Ala Pro Ser Arg Ala Arg Gly Ser Gly Cys
20 25 30
Arg Ala Gly Thr Gly Ala Arg Gly Ala Gly Ala Glu Gly Arg Glu
35 40 45

Gly Glu Ala Cys Gly Thr Val Gly Leu Leu Leu Glu His Ser Phe
50 55 60
Glu Ile Asp Asp Ser Ala Asn Phe Arg Lys Arg Gly Ser Leu Leu
65 70 75
Trp Asn Gln Gln Asp Gly Thr Leu Ser Leu Ser Gln Arg Gln Leu
80 85 90
Ser Glu Glu Glu Arg Gly Arg Leu Arg Asp Val Ala Ala Leu Asn
95 100 105
Gly Leu Tyr Arg Val Arg Ile Pro Arg Arg Pro Gly Ala Leu Asp
110 115 120
Gly Leu Glu Ala Gly Gly Tyr Val Ser Ser Phe Val Pro Ala Cys
125 130 135
Ser Leu Val Glu Ser His Leu Ser Asp Gln Leu Thr Leu His Val
140 145 150
Asp Val Ala Gly Asn Val Val Gly Val Ser Val Val Thr His Pro
155 160 165
Gly Gly Cys Arg Gly His Glu Val Glu Asp Val Asp Leu Glu Leu
170 175 180
Phe Asn Thr Ser Val Gln Leu Gln Pro Pro Thr Thr Ala Pro Gly
185 190 195
Pro Glu Thr Ala Ala Phe Ile Glu Arg Leu Glu Met Glu Gln Ala
200 205 210
Gln Lys Ala Lys Asn Pro Gln Glu Gln Lys Ser Phe Phe Ala Lys
215 220 225
Tyr Trp Met Tyr Ile Ile Pro Val Val Leu Phe Leu Met Met Ser
230 235 240
Gly Ala Pro Asp Thr Gly Gly Gln Gly Gly Gly Gly Gly Gly
245 250 255
Gly Gly Gly Gly Ser Gly Leu Cys Cys Val Pro Pro Ser Leu
260 265

<210> 373
<211> 1706
<212> DNA
<213> Homo sapiens

<400> 373
ggagcgtgc tggaaccga gccggagccg gagccacagc ggggaggggtg 50
gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100
cagcaggtcg tccgggggcc caccatgctg gtgactgcct accttgcttt 150
tgtaggcctc ctggcctcct gcctgggggt ggaactgtca agatgccggg 200

ctaaaccccc tgggaagggcc tgcagcaatc cctccttctc tcggtttcaa 250
ctggacttct atcagggtcta cttcctggcc ctggcagctg attggcttca 300
ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350
aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400
ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450
cctcttctcc ctgacttact cactatgctg cttaaccaaa ctctctcaag 500
actactttgt gctgctagtg gggcgagcac ttgggtgggct gtccacagcc 550
ctgctcttct cagccttcga ggccctggat atccatgagc acgtggaacg 600
gcatgacttc cctgctgagt ggatcccagc tacctttgct cgagctgcct 650
tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700
gccagctgga tagggctggg gcctgtagcg ccctttgtgg ctgccatccc 750
tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800
atgaccggca gcgtgccttc tcaaggacct gtgctggagg cctgcgctgc 850
ctcctgtcgg accgccgctg gctgctgctg ggcaccatac aagctctatt 900
tgagagtgtc atcttcatct ttgtcttctc ctggacacct gtgctggacc 950
cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000
ctgcttggct cttccctgta ccgtatcgcc acctccaaga ggtaccacct 1050
tcagcccatg cacctgctgt cccttgctgt gctcatcgtc gtcttctctc 1100
tcttcatgtt gactttctct accagcccag gccaggagag tccggtggag 1150
tccttcatag cctttctact tattgagttg gcttgtggat tatactttcc 1200
cagcatgagc ttcctacgga gaaaggatgat ccctgagaca gagcaggctg 1250
gtgtactcaa ctgggtcccg gtacctctgc actcactggc ttgcctaggg 1300
ctccttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350
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tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450
gaggagccct atgccctga gctgtaaccc cactccagga caagatagct 1500
gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550
gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600
gggaggacat gatgggggtg atggactgga aagaaggctc caaaagttcc 1650

ctctgtgttta ctccatttta gaaaataaac actttttaaat gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser	1	5	10	15
Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly	20	25	30	
Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe	35	40	45	
Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala	50	55	60	
Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly	65	70	75	
Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu	80	85	90	
Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys	95	100	105	
Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu	110	115	120	
Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala	125	130	135	
Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala	140	145	150	
Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu	155	160	165	
Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val	170	175	180	
Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp	185	190	195	
Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu	200	205	210	
Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn	215	220	225	
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu	230	235	240	

[illegible]

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<210> 376
<211> 188
<212> PRT
<213> Homo sapiens
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<400> 376
Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu
  1                               10                      15
Pro Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu
                20                      25                      30
Tyr Phe Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr
                35                      40                      45
Ala Thr Pro Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr
                50                      55                      60
Glu Gln Ile His Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly
                65                      70                      75
Glu Leu Ser Asn Gly Phe Phe Ile Gln Asp Gln Ile Ala Leu Val
                80                      85                      90

```


Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val Met Ala Gly Val
 1 5 10 15
 Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys
 20 25 30
 Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly
 35 40 45
 Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr
 50 55 60
 Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys
 65 70 75
 Thr Gln Gly Cys Gly Ile Tyr Lys Asp Asn Asn Lys Ser Ser Ile
 80 85 90
 His Cys Met Asp Leu Ser Gln Arg Tyr Cys Leu Met Ala Val Phe
 95 100 105
 Asn Val Ile Tyr Leu Glu Asn Glu Asp Ser Glu
 110 115

<210> 379
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 379
 ctgcctccac tgctctgtgc tggg 24

<210> 380
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 380
 cagagcagtg gatgttcccc tggg 24

<210> 381
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45

<223> Synthetic construct.

<400> 381

ctgaacaaga tggtaagca agtgactggg aaaatgccca tcttc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

ctcgcttctt ccttctggat gggggcccag gggggcccagg agagtataaa 50
 ggcgatgtgg aggggtgccc gcacaaccag acgcccagtc acaggcgaga 100
 gccctgggat gcaaccggcca gagggccatgc tgctgctgct cacgcttgcc 150
 ctcttggggg gccccacctg ggcagggaag atgtatggcc ctggaggagg 200
 caagtatttc agcaccactg aagactacga ccatgaaatc acagggtctgc 250
 ggggtgtctgt aggtcttctc ctggtgaaaa gtgtccagggt gaaacttggg 300
 gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350
 caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400
 ctttctctcg gggatgggtc atgtacacca gcaaggaccg ctatttctat 450
 tttgggaagc ttgatggcca gatctctct gcctaccca gccaaaggagg 500
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 gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600
 ccagttaatc tcacatactc agcaaaactca cccgtgggtc gctaggggtg 650
 ggtatggggc catccgagct gaggccatct gtgtgggtgt ggctgatggt 700
 actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750
 gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met	His	Arg	Pro	Glu	Ala	Met	Leu	Leu	Leu	Leu	Thr	Leu	Ala	Leu
1					5				10					15
Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly
				20					25					30
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr
				35					40					45

Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln
50 55 60
Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly
65 70 75
Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr
80 85 90
Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met
95 100 105
Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly
110 115 120
Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val
125 130 135
Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly
140 145 150
Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro
155 160 165
Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg
170 175

<210> 384
<211> 2379
<212> DNA
<213> Homo sapiens

<400> 384
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agctctgtgg ctgaactggg tgctcatcac ggggaactgct gggctatgga 100
atacagatgt ggcagctcag gtagcccaa attgcctgga agaatacatc 150
atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200
cccctcccca cccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250
atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300
tggtgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350
atgttccaaa atcgggtccat ctcccaaggg gtccaatttt tcttctctggg 400
tgtcagcgag ccctgactca ctacagtgcg gctgacaggg gctgtcatgc 450
aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500
acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag 550
cactggttat agccccact gtcttactga caatgctttc ttctgccgaa 600
cgaggatgcc ctaagggtcg taggtgtgaa ggcaaaatgg tatattgtga 650

atctcagaaa	ttacaggaga	tacctcaag	tatatctgct	ggttgcttag	700
gtttgtccct	tcgctataac	agccttcaaa	aacttaagta	taatcaattt	750
aaagggctca	accagctcac	ctggctatac	cttgaccata	accatatcag	800
caatattgac	gaaaatgctt	ttaatggaat	acgcagactc	aaagagctga	850
ttcttagttc	caatagaatc	tcctattttc	ttaacaatac	cttcagacct	900
gtgacaaatt	tacggaactt	ggatctgtcc	tataatcagc	tgcattctct	950
gggatctgaa	cagtttcggg	gcttgcgga	gctgctgagt	ttacattttac	1000
ggtctaactc	cctgagaacc	atccctgtgc	gaatattcca	agactgccgc	1050
aacctggaac	ttttggacct	gggatataac	cggatccgaa	gtttagccag	1100
gaatgtcttt	gctggcatga	tcagactcaa	agaacttcac	ctggagcaca	1150
atcaattttc	caagctcaac	ctggcccttt	ttccaagggt	ggtcagcctt	1200
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<210> 385
 <211> 513
 <212> PRT
 <213> Homo sapiens

<400> 385
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 20 25 30
 Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val
 35 40 45
 Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser
 50 55 60
 Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys
 65 70 75
 Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu
 80 85 90
 Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe
 95 100 105
 Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg
 110 115 120
 Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu
 125 130 135
 Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser
 140 145 150
 Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg
 155 160 165
 Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys
 170 175 180
 Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser
 185 190 195
 Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu

His Leu Glu His	Asn Gln Phe Ser Lys	Leu Asn Leu Ala Leu Phe
	215	220 225
Pro Arg Leu Val	Ser Leu Gln Asn Leu Tyr	Leu Gln Trp Asn Lys
	230	235 240
Ile Ser Val Ile	Gly Gln Thr Met Ser	Trp Thr Trp Ser Ser Leu
	245	250 255
Gln Arg Leu Asp	Leu Ser Gly Asn Glu	Ile Glu Ala Phe Ser Gly
	260	265 270
Pro Ser Val Phe	Gln Cys Val Pro Asn	Leu Gln Arg Leu Asn Leu
	275	280 285
Asp Ser Asn Lys	Leu Thr Phe Ile Gly	Gln Glu Ile Leu Asp Ser
	290	295 300
Trp Ile Ser Leu	Asn Asp Ile Ser Leu	Ala Gly Asn Ile Trp Glu
	305	310 315
Cys Ser Arg Asn	Ile Cys Ser Leu Val	Asn Trp Leu Lys Ser Phe
	320	325 330
Lys Gly Leu Arg	Glu Asn Thr Ile Ile	Cys Ala Ser Pro Lys Glu
	335	340 345
Leu Gln Gly Val	Asn Val Ile Asp Ala	Val Lys Asn Tyr Ser Ile
	350	355 360
Cys Gly Lys Ser	Thr Thr Glu Arg Phe	Asp Leu Ala Arg Ala Leu
	365	370 375
Pro Lys Pro Thr	Phe Lys Pro Lys Leu	Pro Arg Pro Lys His Glu
	380	385 390
Ser Lys Pro Pro	Leu Pro Pro Thr Val	Gly Ala Thr Glu Pro Gly
	395	400 405
Pro Glu Thr Asp	Ala Asp Ala Glu His	Ile Ser Phe His Lys Ile
	410	415 420
Ile Ala Gly Ser	Val Ala Leu Phe Leu	Ser Val Leu Val Ile Leu
	425	430 435
Leu Val Ile Tyr	Val Ser Trp Lys Arg	Tyr Pro Ala Ser Met Lys
	440	445 450
Gln Leu Gln Gln	Arg Ser Leu Met Arg	Arg His Arg Lys Lys Lys
	455	460 465
Arg Gln Ser Leu	Lys Gln Met Thr Pro	Ser Thr Gln Glu Phe Tyr
	470	475 480
Val Asp Tyr Lys	Pro Thr Asn Thr Glu	Thr Ser Glu Met Leu Leu
	485	490 495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
500 505 510

Cys Glu Val

<210> 386
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 386
ctgggatctg aacagtttcg gggc 24

<210> 387
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 387
ggtccccagg acatggtctg tccc 24

<210> 388
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 388
gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
<211> 1449
<212> DNA
<213> Homo sapiens

<400> 389
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gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150
ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa tggctggtat atctggatcc tctgctgct ggttttgggtg 250
gcagctcttc tctgtggagc tgtggctcctc tgcctccagt gctggctgag 300
gagaccccca attgattctc acaggcgcac catggcagtt tttgctgttg 350
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atgttttggc ccttttaggt cccacctcc atatgaagaa attgtaaaaa 500
caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550
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attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800
gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850
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<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ser	Arg	Ser	Arg	Leu	Phe	Ser	Val	Thr	Ser	Ala	Ile	Ser	Thr
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Ile Gly Ile Leu Cys Leu Pro Leu Phe Gln Leu Val Leu Ser Asp
 20 25 30
 Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln
 35 40 45
 His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Leu Val Leu
 50 55 60
 Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys
 65 70 75
 Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala
 80 85 90
 Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala
 95 100 105
 Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro
 110 115 120
 Asp Leu Tyr Pro Val Pro Ala Pro Cys Phe Gly Pro Leu Gly Ser
 125 130 135
 Pro Pro Pro Tyr Glu Glu Ile Val Lys Thr Thr
 140 145

<210> 391
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 391
 cttttcagtg tcacctcagc gatctc 26

<210> 392
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 392
 ccaaaaacatg gagcaggaac agg 23

<210> 393
 <211> 47
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-47
 <223> Synthetic construct.

<400> 393
 ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394
 <211> 2340
 <212> DNA
 <213> Homo sapiens

<400> 394
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 aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200
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 ttttcaagtc ttgatttgtg gcttacctca agttaccatt tttcagtcaa 400
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 gtcaagttac gtgagcaaat actagactta agcaaaagat atgttaaagc 600
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<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met Phe Phe Thr Ile Ser Arg Lys Asn Met Ser Gln Lys Leu Ser
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Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu
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His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu
35 40 45
Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu
50 55 60
Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser
65 70 75
Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu
80 85 90
Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp
95 100 105
Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr
110 115 120
Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val
125 130 135
Ser Gly Ser Ile Arg
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<210> 396
<211> 2639
<212> DNA
<213> Homo sapiens

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<210> 397
<211> 353
<212> PRT
<213> Homo sapiens

<400> 397
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Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr
20 25 30
Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser
35 40 45
Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr
50 55 60
Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu
65 70 75
Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp
80 85 90
Leu Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser
95 100 105
Arg Leu Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu
110 115 120
Thr Ala Leu Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp
125 130 135
Val Asn Leu Ser His Asn Gln Leu Arg Glu Val Ser Val Ser Ala
140 145 150

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caaccccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

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atgtcattct ctatctattc actgcaagtg cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

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ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

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ccaaaaaaaa aaaaaaaaaa a 1571

<210> 402
<211> 261
<212> PRT
<213> Homo sapiens

<400> 402
Met Arg Gln Phe Pro Lys Thr Ser Phe Asp Ile Ser Pro Glu Met
1 5 10 15
Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu
20 25 30
Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys
35 40 45
Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu
50 55 60
Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu
65 70 75
Leu Leu Trp Ser Pro Asp Phe Arg Pro Lys Met Lys Ala Ser Ser
80 85 90

Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr Leu Leu Trp Thr
 95 100 105
 Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser Cys Val Ile
 110 115 120
 Ala Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Glu Ile Arg
 125 130 135
 Gly Ser Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile Leu
 140 145 150
 Arg Arg Thr Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys
 155 160 165
 Cys Leu Leu Arg His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe
 170 175 180
 Lys Asn Tyr Gln Thr Pro Asp His Tyr Thr Leu Arg Lys Ile Ser
 185 190 195
 Ser Leu Ala Asn Ser Phe Leu Thr Ile Lys Lys Asp Leu Arg Leu
 200 205 210
 Ser His Ala His Met Thr Cys His Cys Gly Glu Glu Ala Met Lys
 215 220 225
 Lys Tyr Ser Gln Ile Leu Ser His Phe Glu Lys Leu Glu Pro Gln
 230 235 240
 Ala Ala Val Val Lys Ala Leu Gly Glu Leu Asp Ile Leu Leu Gln
 245 250 255
 Trp Met Glu Glu Thr Glu
 260

<210> 403
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-28
 <223> Synthetic construct.

<400> 403
 ctcctgtggt ctccagattt caggccta 28

<210> 404
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 404
agtcctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccga ggaggaggag 50
aggcttttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggtaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300
caccgcccat ttacagacac gtagtgtatt ctggaggctg aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tcccctttgg aaatcagtca ttggagggat gatggctggg gttattggcc 450
agtttttagc caatccaact gacctagtga aggttcagat gcaaattgaa 500
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600
gctgggtacc caatatacaa agagcagcac tgggtgaatat gggagattta 650
accacttatg atacagtga acactacttg gtattgaata caccacttga 700
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900
gctttttacc atcttggctg agaatgacct cttggtcaat ggtgttctgg 950
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
Met Ser Val Pro Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
1 5 10 15

Arg Trp Pro Arg Ala Ser Lys Phe Leu Leu Ser Gly Cys Ala Ala
20 25 30

Thr Val Ala Glu Leu Ala Thr Phe Pro Leu Asp Leu Thr Lys Thr
35 40 45

Arg Leu Gln Met Gln Gly Glu Ala Ala Leu Ala Arg Leu Gly Asp
50 55 60

Gly Ala Arg Glu Ser Ala Pro Tyr Arg Gly Met Val Arg Thr Ala
65 70 75

Leu Gly Ile Ile Glu Glu Glu Gly Phe Leu Lys Leu Trp Gln Gly
80 85 90

Val Thr Pro Ala Ile Tyr Arg His Val Val Tyr Ser Gly Gly Arg
95 100 105

Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly Lys Ser
110 115 120

Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly Met
125 130 135

Met Ala Gly Val Ile Gly Gln Phe Leu Ala Asn Pro Thr Asp Leu
140 145 150

Val Lys Val Gln Met Gln Met Glu Gly Lys Arg Lys Leu Glu Gly
155 160 165

Lys Pro Leu Arg Phe Arg Gly Val His His Ala Phe Ala Lys Ile
170 175 180

Leu Ala Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly Trp Val Pro
185 190 195

Asn Ile Gln Arg Ala Ala Leu Val Asn Met Gly Asp Leu Thr Thr
200 205 210

Tyr Asp Thr Val Lys His Tyr Leu Val Leu Asn Thr Pro Leu Glu
215 220 225

Asp Asn Ile Met Thr His Gly Leu Ser Ser Leu Cys Ser Gly Leu
230 235 240

Val Ala Ser Ile Leu Gly Thr Pro Ala Asp Val Ile Lys Ser Arg
245 250 255

Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr
260 265 270

Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly
275 280 285

Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met
290 295 300

Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg

305

310

315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407
<211> 31
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-31
<223> Synthetic construct.

<400> 407
cgcgatccc gttatcgtct tgcgctactg c 31

<210> 408
<211> 34
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-34
<223> Synthetic construct.

<400> 408
gcggaattct taaaatggac tgactccact catc 34

<210> 409
<211> 1487
<212> DNA
<213> Homo sapiens

<400> 409
cggacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50
tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100
cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150
tagataattt tcgttggcca gaatgtgaat gtattgactg gagtggagaga 200
agaaatgctg tggcatctgt tgcgcaggt atattgtttt ttacaggctg 250
gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300
accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcatg 350
ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400
ctgttttagga agaacaggtg ctcgagtttg gcttttcatt ggtttcatgt 450
tgatgttttg gtcacttatt gcttccatgt ggattctttt tgggtgcatat 500
gttaccctaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550

tgcacttata ttttttagca ctctgatcta caaatttggga agaaccgaag 600
 agctatggac ctgagatcac ttcttaagtc acatttttcct tttgttatat 650
 tctgttttga gataggtttt ttatctctca gtacacattg ccaaattggag 700
 tagattgtac attaaatggt ttgtttcttt acatttttat gttctgagtt 750
 ttgaaatagt tttatgaaat ttctttatatt ttcattgcat agactgttaa 800
 tatgtatata atacaagact atatgaattg gataatgagt atcagttttt 850
 tattcctgag atttagaact tgatctactc cctgagccag gggttacatca 900
 tcttgtcatt ttagaagtaa ccactcttgt ctctctgggt gggcacggtg 950
 gctcatgcct gtaatcccag cactttggga ggccgaggcg ggccgattgc 1000
 ttgagggtcaa gtgtttgaga ccagcctggc caacatggcg aaaccccatc 1050
 tactaaaaat acaaaaatta gccaggcatg gtggtgggtg cctgtaatcc 1100
 cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150
 aggttgcaat gagctgagtt tgcgccactg cactctagcc tggggggagaa 1200
 agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250
 gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300
 cataaaaggt tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350
 ttttttggtg aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400
 tttatataat gattttttta atgcccaaag gactagtttg aaagcttctt 1450
 ttaaaaagaa ttcctcta atgactttat gtgagaa 1487

<210> 410
 <211> 158
 <212> PRT
 <213> Homo sapiens

<400> 410
 Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys
 1 5 10 15
 Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala
 20 25 30
 Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala
 35 40 45
 Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr
 50 55 60
 Cys Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val
 65 70 75

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu
80 85 90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu
95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala
110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe
125 130 135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe
140 145 150

Gly Arg Thr Glu Glu Leu Trp Thr
155

<210> 411
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.

<400> 411
gtttgaggaa gctgggatac 20

<210> 412
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.

<400> 412
ccaaactcga gcacctgttc 20

<210> 413
<211> 40
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 413
atggcaggct tctagataa ttttcgttgg ccagaatgtg 40

<210> 414

<211> 1337
<212> DNA
<213> Homo sapiens

<400> 414
gttgatggca aacttcctca aaggaggggc agagcctgagc cagggcagga 50
gcagctggcc cactggcgcc ccgcaacact ccgtctcacc ctctggggccc 100
actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150
gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200
gggacctacg gcacctgctg gaccacctcg ctttctccat cgaagcaggg 250
aagtgggagc ctgagaccct cgggtggaag ctgaccccaa gccacccttc 300
acctggacag gatgagagtg tcaggtgtgc ttgcgcctct ggccctcatc 350
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500
aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtggggccc 550
tactatgtgc tttgaagacc gcatgatcat gagtccctgtg aaaaacaatg 600
tgggcaagag cctaaacatc gccctggtga atggaaccac gggagctgtg 650
ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700
gaaattcctt aaagaaattc cggggggtgc actggtgctg gtggcctcct 750
acgacgatcc agggaccaa atgaacgatg aaagcaggaa actcttctct 800
gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850
cttcatagga gccaaagacc tcaggggtaa aagccccctt gagcagttct 900
taaagaacag ccagacaca aacaaatacg agggatggcc agagctgctg 950
gagatggagg gctgcatgcc ccggaagcca ttttaggggt gctgtggctc 1000
ttctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050
cccggcaggg gctgaggagg aggagcaggg ggtgctgctg ggaagggtgct 1100
gcaggtcctt gcacgtgtg tcgcgcctct cctcctcgga aacagaaccc 1150
tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200
accagctgtc tgtggagaga atggggtgct ttcgtcaggg actgctgacg 1250
gctggtcctg aggaaggaca aactgcccag acttgagccc aattaaattt 1300
tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 415
 Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
 1 5 10 15
 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
 20 25 30
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
 35 40 45
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
 50 55 60
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
 65 70 75
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
 80 85 90
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
 95 100 105
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
 110 115 120
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
 125 130 135
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
 140 145 150
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
 155 160 165
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
 170 175 180
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
 185 190 195
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
 200 205 210
 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
 215 220

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-21
<223> Synthetic construct.

<400> 416
gccatagtca cgacatggat g 21

<210> 417
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 417
ggatggccag agctgctg 18

<210> 418
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 418
aaagtacaag tgtggcctca tcaagc 26

<210> 419
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 419
tctgactcct aagtcaggca ggag 24

<210> 420
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 420
attctctcca cagacagctg gttc 24

<210> 421
 <211> 46
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-46
 <223> Synthetic construct.

<400> 421
 gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422
 <211> 1701
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 1528
 <223> unknown base

<400> 422
 gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
 tgtcctgagg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100
 tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150
 cagccagga gctcgtctgc tctctctctc tctctctcac tctccctcc 200
 ctctctctct gctgtctcta gtctcttagt cctcaaattc ccagtcccct 250
 gcaccccttc ctgggacact atgttgttct ccgccctcct gctggagggtg 300
 atttggatcc tggctgcaga tgggggtcaa cactggacgt atgagggccc 350
 acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400
 cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
 ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500
 ggacctgcac aacaatggcc acacagtgc actctctctg ccctctaccc 550
 tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600
 cactgggggtc agaaaggatc cccagggggg tcagaacacc agatcaacag 650
 tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700
 atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750
 ggcacccata ttgaggtggg tgagactaag aatatagctt atgaacacat 800
 tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtaattc 900
cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950
gacagttttt tatagaaggt cccagatttc aatggaacag ctggaaaagc 1000
ttcagggggac attgttctcc acagaagagg agccctctaa gcttctggta 1050
cagaactacc gagcccttca gcctctcaat cagcgcatgg tctttgcttc 1100
tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150
gtgtaggaat cttgggttggc tgtctctgcc ttctcctggc tgtttatttc 1200
attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtggt 1250
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catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg 1350
gggtgtagga tctggccaga aacactgtag gagtagtaag cagatgtcct 1400
ccttccccctg gacatctctt agagaggaat ggaccagggc tgtcattcca 1450
ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500
gaaatcgctg tgttggttaat gcagaganca aactctgttt agttgcaggg 1550
gaagtttggg atatacccca aagtcctcta cccctcact tttatggccc 1600
tttccttaga tatactgcgg gatctctcct taggataaag agttgctgtt 1650
gaagttgtat atttttgatc aatatatttg gaaattaaag tttctgactt 1700
t 1701

<210> 423
<211> 337
<212> PRT
<213> Homo sapiens

<400> 423
Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala
1 5 10 15
Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln
20 25 30
Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln
35 40 45
Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp
50 55 60
Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu
65 70 75
Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

80	85	90
Pro Ser Thr Leu Tyr Leu Gly Gly Leu	Pro Arg Lys Tyr Val	Ala
95	100	105
Ala Gln Leu His Leu His Trp Gly Gln	Lys Gly Ser Pro Gly	Gly
110	115	120
Ser Glu His Gln Ile Asn Ser Glu Ala	Thr Phe Ala Glu Leu	His
125	130	135
Ile Val His Tyr Asp Ser Asp Ser Tyr	Asp Ser Leu Ser Glu	Ala
140	145	150
Ala Glu Arg Pro Gln Gly Leu Ala Val	Leu Gly Ile Leu Ile	Glu
155	160	165
Val Gly Glu Thr Lys Asn Ile Ala Tyr	Glu His Ile Leu Ser	His
170	175	180
Leu His Glu Val Arg His Lys Asp Gln	Lys Thr Ser Val Pro	Pro
185	190	195
Phe Asn Leu Arg Glu Leu Leu Pro Lys	Gln Leu Gly Gln Tyr	Phe
200	205	210
Arg Tyr Asn Gly Ser Leu Thr Thr Pro	Pro Cys Tyr Gln Ser	Val
215	220	225
Leu Trp Thr Val Phe Tyr Arg Arg Ser	Gln Ile Ser Met Glu	Gln
230	235	240
Leu Glu Lys Leu Gln Gly Thr Leu Phe	Ser Thr Glu Glu Glu	Pro
245	250	255
Ser Lys Leu Leu Val Gln Asn Tyr Arg	Ala Leu Gln Pro Leu	Asn
260	265	270
Gln Arg Met Val Phe Ala Ser Phe Ile	Gln Ala Gly Ser Ser	Tyr
275	280	285
Thr Thr Gly Glu Met Leu Ser Leu Gly	Val Gly Ile Leu Val	Gly
290	295	300
Cys Leu Cys Leu Leu Leu Ala Val Tyr	Phe Ile Ala Arg Lys	Ile
305	310	315
Arg Lys Lys Arg Leu Glu Asn Arg Lys	Ser Val Val Phe Thr	Ser
320	325	330
Ala Gln Ala Thr Thr Glu Ala		
335		

<210> 424
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 424
 gtaaagtcgc tggccagc 18

<210> 425
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 425
 ccgatctgc ctgctgta 18

<210> 426
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 426
 ctgcactgta tggccattat tgtg 24

<210> 427
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 427
 cagaaacca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428
 <211> 1073
 <212> DNA
 <213> Homo sapiens

<400> 428
 aatttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50
 acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100
 gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

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aacctgcttt gggactccct cccacaaaac tggctccgga tcagggaaca 200
ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250
accattaaca cagatgctca cactggggcc agatctgcat ctgttaaata 300
ctgctgcagg aatgacacct ggtaccaga cccaccatt gaccctggga 350
gggttgaatg tacaacagca actgcacca catgtgttac caatttttgt 400
cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
aaatcttcac gagcctcatc atccattcct tgttcccggg aggcacctg 500
cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550
agcaggagga gcaggtgtaa atcctgccac ccagggaacc ccagcaggcc 600
gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650
gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaata 700
agcaaatgga attcagtaag ctgtttcaaa ttttttcaac taagctgcct 750
cgaatttggt gatacatgtg aatctttatc attgattata ttatggaata 800
gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900
cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950
tatgctgcct ggatgatatg catattaaaa catatttgga aaactggaaa 1000
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050
aaaaaaaaaa aaaaaaaaaa aaa 1073

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<210> 429
 <211> 209
 <212> PRT
 <213> Homo sapiens

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<400> 429
Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg
 1          5          10          15
Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys
          20          25          30
Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn
          35          40          45
Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu
          50          55          60
Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met
          65          70          75

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Thr Pro Gly Thr Gln Thr His Pro Leu Thr Leu Gly Gly Leu Asn
80 85 90

Val Gln Gln Gln Leu His Pro His Val Leu Pro Ile Phe Val Thr
95 100 105

Gln Leu Gly Ala Gln Gly Thr Ile Leu Ser Ser Glu Glu Leu Pro
110 115 120

Gln Ile Phe Thr Ser Leu Ile Ile His Ser Leu Phe Pro Gly Gly
125 130 135

Ile Leu Pro Thr Ser Gln Ala Gly Ala Asn Pro Asp Val Gln Asp
140 145 150

Gly Ser Leu Pro Ala Gly Gly Ala Gly Val Asn Pro Ala Thr Gln
155 160 165

Gly Thr Pro Ala Gly Arg Leu Pro Thr Pro Ser Gly Thr Asp Asp
170 175 180

Asp Phe Ala Val Thr Thr Pro Ala Gly Ile Gln Arg Ser Thr His
185 190 195

Ala Ile Glu Glu Ala Thr Thr Glu Ser Ala Asn Gly Ile Gln
200 205

<210> 430
<211> 1257
<212> DNA
<213> Homo Sapien

<400> 430
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cggagcgcgg cggagccaga cgctgaccac gttcctctcc tcggtctcct 100
ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
gccccgccgc ctccccgcag cggctccgcg gcctcctgct gctcctgctg 200
ctgcagctgc ccgcgccgtc gagcgctctt gagatcccca aggggaagca 250
aaaggcgcag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacaccca 450
actacaagca gtgttcatgg agttcattga attatggcat agatcttggg 500
aaaattgcgg agtgtacatt tacaaagatg cgttcaaata gtgctctaag 550
agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600
agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650

attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700
aattaatatt catcgcaactt cttctgtgga aggactttgt gaaggaattg 750
gtgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac 800
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850
tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900
ttattatgcc ttggaatggt tcacttaaata gacattttta ataagtttat 950
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000
tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050
aagtggtttc aatatttttt ttagttgggt agaatacttt cttcatagtc 1100
acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150
ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200
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tccaaca 1257

<210> 431
<211> 243
<212> PRT
<213> Homo Sapien

<400> 431
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1 5 10 15
Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
20 25 30
Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
35 40 45
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
50 55 60
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
65 70 75
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
95 100 105
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
110 115 120
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
140 145 150
Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
155 160 165
Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
170 175 180
Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
185 190 195
Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
200 205 210
Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
215 220 225
Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
230 235 240

Leu Pro Lys

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<213> Artificial Sequence

<220>
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aggacttgcc ctcaggaa 18

<210> 433
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<220>
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<400> 433
cgcaggacag ttgtgaaaat a 21

<210> 434
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<220>
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<400> 434
atgacgctcg tccaaggcca c 21

<210> 435

<211> 19
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<220>
<223> Synthetic oligonucleotide probe

<400> 435
cccacctgta ccaccatgt 19

<210> 436
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<212> DNA
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<400> 436
actccaggca ccatctgttc tccc 24

<210> 437
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<400> 437
aagggtggc attcaagtc 19

<210> 438
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<400> 438
tgacctggca aaggaagaa 19

<210> 439
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<220>
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<400> 439
cagccaccct ccagtccaag g 21

<210> 440
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<400> 440
gggtcgtgtt ttggagaga 19
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<211> 20
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<213> Artificial Sequence
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<220>
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ctggcaggag ttaaagttcc aaqa 24
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aaaggacacc gggatgtg 18
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<210> 445
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<213> Artificial Sequence
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<220>
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<210> 446
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<400> 446
caattctgga tgagggtgga ga 22

<210> 447
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caggactgag cgcttggtta 20

<210> 448
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<212> DNA
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<220>
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caaagcgcca agtaccggac c 21

<210> 449
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ccagacctca gccaggaa 18

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ccctagctga ccccttca 18

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<210> 452
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<212> DNA
<213> Artificial Sequence

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<400> 452
ctctccccct cccttttcct ttgttt 26

<210> 453
<211> 18
<212> DNA
<213> Artificial Sequence

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<400> 453
ctctggtgcc cacagtga 18

<210> 454
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<210> 455
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<400> 455
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<210> 456
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ccttgaaaag gacccagttt 20

<210> 457

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 458

<211> 18

<212> DNA

<213> Artificial Sequence

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<210> 459

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<210> 460

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<223> Synthetic oligonucleotide probe

<400> 460
tgctaggcga cgacacccag acc 23

<210> 461

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 461
tggacacgtg gcagtgga 18

<210> 462
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<220>
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<400> 462
tcatggtctc gtccattc 19

<210> 463
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<400> 463
caccatttgt ttctctgtct ccccatc 27

<210> 464
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<400> 464
ccggcatcct tggagtag 18

<210> 465
<211> 20
<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 465
tccccattag cacaggagta 20

<210> 466
<211> 23
<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 466

aggctcttgc ctgtcctgct gct 23

<210> 467

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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gcccagagtc ccacttgt 18

<210> 468

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<400> 468

actgctccgc ctactacga 19

<210> 469

<211> 20

<212> DNA

<213> Artificial Sequence

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<400> 469

aggcatcctc gccgtcctca 20

<210> 470

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 470

aaggccaagg tgagtccat 19

<210> 471

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 471

cgagtgtgtg cgaaacctaa 20

<210> 472

<211> 24
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<220>
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<400> 472
tcagggtcta catcagcctc ctgc 24

<210> 473
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<212> DNA
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<400> 473
aaggccaagg tgagtccat 19

<210> 474
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<212> DNA
<213> Artificial Sequence

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<400> 474
cctactgagg agccctatgc 20

<210> 475
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 475
tccaggtgga ccccacttca gg 22

<210> 476
<211> 24
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 476
gggaggctta taggcccaat ctgg 24

<210> 477
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<223> Synthetic oligonucleotide probe

<400> 477

ggcttcagca gcacgtgtga agtcgaagtc gcagtcacag atatcaatga 50